

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Maassab, Hunein F
Herlocher, Martha L

(ii) TITLE OF INVENTION: Cold-adapted Influenza Virus

(iii) NUMBER OF SEQUENCES: 40

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Anna M Lewak
- (B) STREET: 5445 Corporate Drive
- (C) CITY: Troy
- (D) STATE: MI
- (E) COUNTRY: USA
- (F) ZIP: 48098

RECEIVED
03 1993
GROUP 1800

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US
- (B) FILING DATE:
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Lewak, Anna M
- (B) REGISTRATION NUMBER: 33006

(C) REFERENCE/DOCKET NUMBER: 2115-00257

a/
(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 313-641-1600
- (B) TELEFAX: 313-641-0270

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 890 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: NS

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 27..56
- (D) OTHER INFORMATION: /product= "nonstructural protein NS2"
/gene= "NS"
/note= "nonstructural protein NS2"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(483, "a")

G1
(D) OTHER INFORMATION: /note= "a in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: exon
(B) LOCATION: 529..861
(D) OTHER INFORMATION: /product= "nonstructural protein NS2"
/gene= "NS"
/note= "nonstructural protein NS2"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict
(B) LOCATION: replace(813, "g")
(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: join(27..56, 529..861)
(D) OTHER INFORMATION: /product= "nonstructural protein NS2"
/gene= "NS"
/note= "nonstructural protein NS2"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 27..677
(D) OTHER INFORMATION: /product= "nonstructural protein NS1"
/gene= "NS"
/note= "nonstructural protein NS1"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

- Q1
- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
- (B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) influenza virus
- (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
- (G) DATE: 1993
- (K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 890

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C
- (B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza vaccine strain, A/Ann Arbor/6/60(H2N2)
- (C) JOURNAL: Virology
- (D) VOLUME: 167
- (F) PAGES: 554-567
- (G) DATE: 1988
- (K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCAAAAGCA GGGUGACAAA GACAUA AUG GAU CCU AAC ACU GUG UCA AGC UUU Met Asp Pro Asn Thr Val Ser Ser Phe	53
1 5	
CAG GUA GAU UGC UUC CUU UGG CAU GUC CGC AAA CAA GUU GCA GAC CAA Gln Val Asp Cys Phe Leu Trp His Val Arg Lys Gln Val Ala Asp Gln	101
10 15 20 25	
GAA CUA GGU GAU GCC CCA UUC CUU GAU CGG CUU CGC CGA GAU CAG AAG Glu Leu Gly Asp Ala Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys	149
30 35 40	
UCC CUA AGG GGA AGA GGC AGU ACU CUC GGU CUG AAC AUC GAA ACA GCC Ser Leu Arg Gly Arg Gly Ser Thr Leu Gly Leu Asn Ile Glu Thr Ala	197
45 50 55	

ACC CGU GUU GGA AAG CAG AUA GUG GAG AGG AUU CUG AAG GAA GAA UCC 245
Thr Arg Val Gly Lys Glu Ile Val Glu Arg Ile Leu Lys Glu Glu Ser
60 65 70

GAU GAG GCA CUU AAA AUG ACC AUG GCC UCC GCA CCU GCU UCG CGA UAC 293
Asp Glu Ala Leu Lys Met Thr Met Ala Ser Ala Pro Ala Ser Arg Tyr
75 80 85

CUA ACU GAC AUG ACU AUU GAG GAA AUG UCA AGG GAC UGG UUC AUG CUA 341
Leu Thr Asp Met Thr Ile Glu Glu Met Ser Arg Asp Trp Phe Met Leu
90 95 100 105

AUG CCC AAG CAG AAA GUG GCA GGC CCU CUU UGU AUC AGC AUG GAC CAG 389
Met Pro Lys Glu Lys Val Ala Gly Pro Leu Cys Ile Arg Met Asp Glu
110 115 120

GCA AUC AUG GAU AAG AAC AUC AUA UUG AAA GCG AAU UUC AGU GUG AUU 437
Ala Ile Met Asp Lys Asn Ile Ile Leu Lys Ala Asn Phe Ser Val Ile
125 130 135

UUU GAC CGG CUA GAG ACC CUA AUA UUA CUA AGG GCU UUC ACC GAA ACG 485
Phe Asp Arg Leu Glu Thr Leu Ile Leu Leu Arg Ala Phe Thr Glu Thr
140 145 150

GGA GCA AUU GUU GGC GAA AUU UCA CCA UUG CCU UCU CUU CCA GGA CAU 533
Gly Ala Ile Val Gly Glu Ile Ser Pro Leu Pro Ser Leu Pro Gly His
155 160 165

ACU AAU GAG GAU GUC AAA AAU GCA AUU GGG GUC CUC AUC GGA GGA CUU 581
Thr Asn Glu Asp Val Lys Asn Ala Ile Gly Val Leu Ile Gly Gly Leu
170 175 180 185

GAA UGG AAU GAU AAC ACA GUU CGA GUC UCU AAA ACU CUA CAG AGA UUC 629
Glu Trp Asn Asp Asn Thr Val Arg Val Ser Lys Thr Leu Glu Arg Phe
190 195 200

GCU UGG AGA AGC AGU GAU GAG AAU GGG AGA CCU CCA CUC ACU CCA AAA 677
Ala Trp Arg Ser Ser Asp Glu Asn Gly Arg Pro Pro Leu Thr Pro Lys
205 210 215

UAGAAACGGA AAAUGGCGAG AACAAUUAGG UCAAAAGUUC GAAGAAAUA GAUGGCUGAU 737

UGAAGAAGUG AGACACAAAU UGAAGAUAC AGAGAAUAGU UUUGAGCAA UAACAUUUAU 797

GCAAGCCUUA CAGCUGCUAU UUGAAGUGGA ACAAGAGAUA AGAACUUUCU CGUUUCAGCU 857

UAUUUAAUGA UAAAAAACAC CCUUGUUUCU ACU 890

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

A1
(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys Phe Leu Trp
1 5 10 15

His Val Arg Lys Gln Val Ala Asp Gln Glu Leu Gly Asp Ala Pro Phe
20 25 30

Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly Arg Gly Ser
35 40 45

Thr Leu Gly Leu Asn Ile Glu Thr Ala Thr Arg Val Gly Lys Gln Ile
50 55 60

Val Glu Arg Ile Leu Lys Glu Glu Ser Asp Glu Ala Leu Lys Met Thr
65 70 75 80

Met Ala Ser Ala Pro Ala Ser Arg Tyr Leu Thr Asp Met Thr Ile Glu
85 90 95

Glu Met Ser Arg Asp Trp Phe Met Leu Met Pro Lys Gln Lys Val Ala
100 105 110

Gly Pro Leu Cys Ile Arg Met Asp Gln Ala Ile Met Asp Lys Asn Ile
115 120 125

Ile Leu Lys Ala Asn Phe Ser Val Ile Phe Asp Arg Leu Glu Thr Leu
130 135 140

Ile Leu Leu Arg Ala Phe Thr Glu Thr Gly Ala Ile Val Gly Glu Ile
145 150 155 160

Ser Pro Leu Pro Ser Leu Pro Gly His Thr Asn Glu Asp Val Lys Asn
165 170 175

Ala Ile Gly Val Leu Ile Gly Gly Leu Glu Trp Asn Asp Asn Thr Val
180 185 190

Arg Val Ser Lys Thr Leu Gln Arg Phe Ala Trp Arg Ser Ser Asp Glu
195 200 205

Asn Gly Arg Pro Pro Leu Thr Pro Lys
210 215

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- a1
(A) LENGTH: 418 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 27..389
(D) OTHER INFORMATION: /product= "Nonstructural protein 2"
/gene= "NS2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCAAAAGCA GGGUGACAAA GACAUA AUG GAU CCU AAC ACU GUG UCA AGC UUU Met Asp Pro Asn Thr Val Ser Ser Phe 1 5	53
CAG GAC AUA CUA AUG AGG AUG UCA AAA AUG CAA UUG GGG UCC UCA UCG Gln Asp Ile Leu Met Arg Met Ser Lys Met Gln Leu Gly Ser Ser Ser 10 15 20 25	101
GAG GAC UUG AAU GGA AUG AUA ACA CAG UUC GAG UCU CUA AAA CUC UAC Glu Asp Leu Asn Gly Met Ile Thr Gln Phe Glu Ser Leu Lys Leu Tyr 30 35 40	149
AGA GAU UCG CUU GGA GAA GCA GUG AUG AGA AUG GGA GAC CUC CAC UCA Arg Asp Ser Leu Gly Glu Ala Val Met Arg Met Gly Asp Leu His Ser 45 50 55	197
CUC CAA AAU AGA AAC GGA AAA UGG CGA GAA CAA UUA GGU CAA AAG UUC Leu Gln Asn Arg Asn Gly Lys Trp Arg Glu Gln Leu Gly Gln Lys Phe 60 65 70	245
GAA GAA AUA AGA UGG CUG AUU GAA GAA GUG AGA CAC AAA UUG AAG AUA Glu Glu Ile Arg Trp Leu Ile Glu Glu Val Arg His Lys Leu Lys Ile 75 80 85	293
ACA GAG AAU AGU UUU GAG CAA AUA ACA UUU AUG CAA GCC UUA CAG CUG Thr Glu Asn Ser Phe Glu Gln Ile Thr Phe Met Gln Ala Leu Gln Leu 90 95 100 105	341

CUA UUU GAA GUG GAA CAA GAG AUA AGA ACU UUC UCG UUU CAG CUU AUU
Leu Phe Glu Val Glu Gln Glu Ile Arg Thr Phe Ser Phe Gln Leu Ile
110 115 120
A!
UAAAUGAUAAA AAACACCCUU GUUUCUACU 389
418

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Pro Asn Thr Val Ser Ser Phe Gln Asp Ile Leu Met Arg Met
1 5 10 15
Ser Lys Met Gln Leu Gly Ser Ser Ser Glu Asp Leu Asn Gly Met Ile
20 25 30
Thr Gln Phe Glu Ser Leu Lys Leu Tyr Arg Asp Ser Leu Gly Glu Ala
35 40 45
Val Met Arg Met Gly Asp Leu His Ser Leu Gln Asn Arg Asn Gly Lys
50 55 60
Trp Arg Glu Gln Leu Gly Gln Lys Phe Glu Glu Ile Arg Trp Leu Ile
65 70 75 80
Glu Glu Val Arg His Lys Leu Lys Ile Thr Glu Asn Ser Phe Glu Gln
85 90 95
Ile Thr Phe Met Gln Ala Leu Gln Leu Leu Phe Glu Val Glu Gln Glu
100 105 110
Ile Arg Thr Phe Ser Phe Gln Leu Ile
115 120

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs

- u
- (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: RNA (genomic)
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Influenza virus
 - (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)
- (vii) IMMEDIATE SOURCE:
- (B) CLONE: M
- (ix) FEATURE:
- (A) NAME/KEY: exon
 - (B) LOCATION: 26..51
 - (D) OTHER INFORMATION: /product= "matrix protein M2"
/gene= "M"
/note= "matrix protein M2"
/citation= ([1][2])
- (ix) FEATURE:
- (A) NAME/KEY: exon
 - (B) LOCATION: 740..1004
 - (D) OTHER INFORMATION: /product= "matrix protein M2" /gene= "M"
/note= "matrix protein M2"
/citation= ([1][2])
- (ix) FEATURE:
- (A) NAME/KEY: conflict
 - (B) LOCATION: replace(969, "u")
 - (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3)"
/citation= ([1][2])

a1
(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(26..51, 740..1004)
- (D) OTHER INFORMATION: /product= "matrix protein M2"
/gene= "M"
/note= "matrix protein M2"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 26..781
- (D) OTHER INFORMATION: /product= "matrix protein M1"
/gene= "M"
/note= "matrix protein M1"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
- (B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) influenza virus
- (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
- (G) DATE: 1993
- (K) RELEVANT RESIDUES IN SEQ ID NO:5: FROM 1 TO 1027

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C
- (B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza vaccine strain, A/Ann Arbor/6/60(H2N2)
- (C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-557

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:5: FROM 1 TO 1027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGCAAAAGCA GGUAGAUUU GAAAG AUG AGU CUU CUA ACC GAG GUC GAA ACG Met Ser Leu Leu Thr Glu Val Glu Thr	52
1 5	
UAC GUU CUC UCU AUC AUC CCG UCA GGC CCC CUC AAA GCC GAG AUC GCA Tyr Val Leu Ser Ile Ile Pro Ser Gly Pro Leu Lys Ala Glu Ile Ala	100
10 15 20 25	
CAG AGA CUU GAA GAU GUC UUU GCU GGG AAA AAC ACC GAU CUU GAG GCU Gln Arg Leu Glu Asp Val Phe Ala Gly Lys Asn Thr Asp Leu Glu Ala	148
30 35 40	
CUC AUG GAA UGG CUA AAG ACA AGA CCA AUC CUG UCA CCU CUG ACU AAG Leu Met Glu Trp Leu Lys Thr Arg Pro Ile Leu Ser Pro Leu Thr Lys	196
45 50 55	
GGG AUU UUG GGA UUU GUA UUC ACG CUC ACC GUG CCC AGU GAG CGA GGA Gly Ile Leu Gly Phe Val Phe Thr Leu Thr Val Pro Ser Glu Arg Gly	244
60 65 70	
CUG CAG CGU AGA CGC UUU GUC CAA AAU GCC CUC AAU GGG AAU GGG GAU Leu Gln Arg Arg Phe Val Gln Asn Ala Leu Asn Gly Asn Gly Asp	292
75 80 85	
CCA AAU AAC AUG GAC AGA GCA GUU AAA CUG UAU AGA AAG CUU AAG AGG Pro Asn Asn Met Asp Arg Ala Val Lys Leu Tyr Arg Lys Leu Lys Arg	340
90 95 100 105	
GAG AUA ACA UUC CAU GGG GCC AAA GAA AUA GCG CUC AGU UAU UCU GCU Glu Ile Thr Phe His Gly Ala Lys Glu Ile Ala Leu Ser Tyr Ser Ala	388
110 115 120	
GGU GCA CUU GCC AGU UGU AUG GGC CUC AUA UAC AAC AGG AUG GGG GCU Gly Ala Leu Ala Ser Cys Met Gly Leu Ile Tyr Asn Arg Met Gly Ala	436
125 130 135	
GUG ACC ACU GAA GUG GUC UUA GGC CUG GUA UGU GCA ACC UGU GAA CAG Val Thr Thr Glu Val Val Leu Gly Leu Val Cys Ala Thr Cys Glu Gln	484
140 145 150	
AUU GCU GAC UCC CAG CAU AGG UCU CAU AGG CAA AUG GUG ACA ACA ACC Ile Ala Asp Ser Gln His Arg Ser His Arg Gln Met Val Thr Thr Thr	532
155 160 165	

A
AAU CCA CUA AUA AGA CAU GAG AAC AGA AUG GUU CUG GCC AGC ACU ACA 580
Asn Pro Leu Ile Arg His Glu Asn Arg Met Val Leu Ala Ser Thr Thr
170 175 180 185

GCU AAG GCU AUG GAG CAA AUG GCU GGA UCG AGU GAG CAA GCA GCA GAG 628
Ala Lys Ala Met Glu Gln Met Ala Gly Ser Ser Glu Gln Ala Ala Glu
190 195 200

GCC AUG GAG GUU GCU AGU CAG GCC AGG CAA AUG GUG CAG GCA AUG AGA 676
Ala Met Glu Val Ala Ser Gln Ala Arg Gln Met Val Gln Ala Met Arg
205 210 215

GUU AUU GGG ACU CAU CCU AGC UCC AGU GCU GGU CUA AAA AAU GAU CUU 724
Val Ile Gly Thr His Pro Ser Ser Ala Gly Leu Lys Asn Asp Leu
220 225 230

CUU GAA AAU UUG CAG GCC UAU CAG AAA CGA AUG GGG GUG CAG AUG CAA 772
Leu Glu Asn Leu Gln Ala Tyr Gln Lys Arg Met Gly Val Gln Met Gln
235 240 245

CGA UUC AAG UGACCCUCUU GUUGUUGCCG CGAGUAUCAU UGGGAUCUUG 821
Arg Phe Lys
250

CACUUGAUAU UGUGGAUUCU UGAUCAUCUU UUUUCAAAAU GCAUUUAUCG CUUCUUUAAA 881
CACGGUCUGA AAAGAGGGCC UUCUACGGAA GGAGUACCAG AGUCUAUGAG GGAAGAAUAU 941
CGAAAGGAAC AGCAGAGUGC UGUGGAUUCU GACGAUAGUC AUUUUGUCAG CAUAGAGCUG 1001
GAGUAAAAAA CUACCUUGUU UCUACU 1027

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Leu Leu Thr Glu Val Glu Thr Tyr Val Leu Ser Ile Ile Pro
1 5 10 15

Ser Gly Pro Leu Lys Ala Glu Ile Ala Gln Arg Leu Glu Asp Val Phe
20 25 30

Ala Gly Lys Asn Thr Asp Leu Glu Ala Leu Met Glu Trp Leu Lys Thr
35 40 45

Arg Pro Ile Leu Ser Pro Leu Thr Lys Gly Ile Leu Gly Phe Val Phe
50 55 60

Thr Leu Thr Val Pro Ser Glu Arg Gly Leu Gln Arg Arg Arg Phe Val
65 70 75 80

Gln Asn Ala Leu Asn Gly Asn Gly Asp Pro Asn Asn Met Asp Arg Ala
85 90 95

Val Lys Leu Tyr Arg Lys Leu Lys Arg Glu Ile Thr Phe His Gly Ala
100 105 110

Lys Glu Ile Ala Leu Ser Tyr Ser Ala Gly Ala Leu Ala Ser Cys Met
115 120 125

Gly Leu Ile Tyr Asn Arg Met Gly Ala Val Thr Thr Glu Val Val Leu
130 135 140

Gly Leu Val Cys Ala Thr Cys Glu Gln Ile Ala Asp Ser Gln His Arg
145 150 155 160

Ser His Arg Gln Met Val Thr Thr Asn Pro Leu Ile Arg His Glu
165 170 175

Asn Arg Met Val Leu Ala Ser Thr Thr Ala Lys Ala Met Glu Gln Met
180 185 190

Ala Gly Ser Ser Glu Gln Ala Ala Glu Ala Met Glu Val Ala Ser Gln
195 200 205

Ala Arg Gln Met Val Gln Ala Met Arg Val Ile Gly Thr His Pro Ser
210 215 220

Ser Ser Ala Gly Leu Lys Asn Asp Leu Leu Glu Asn Leu Gln Ala Tyr
225 230 235 240

Gln Lys Arg Met Gly Val Gln Met Gln Arg Phe Lys
245 250

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

a
(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 26..316
- (D) OTHER INFORMATION: /product= "Matrix M2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGCAAAAGCA GGUAGAUUU GAAAG AUG AGU CUU CUA ACC GAG GUC GAA ACG	52
Met Ser Leu Leu Thr Glu Val Glu Thr	
1 5	
CCU AUC AGA AAC GAA UGG GGG UGC AGA UGC AAC GAU UCA AGU GAC CCU	100
Pro Ile Arg Asn Glu Trp Gly Cys Arg Cys Asn Asp Ser Ser Asp Pro	
10 15 20 25	
CUU GUU GUU GCC GCG AGU AUC AUU GGG AUC UUG CAC UUG AUA UUG UGG	148
Leu Val Val Ala Ala Ser Ile Ile Gly Ile Leu His Leu Ile Leu Trp	
30 35 40	
AUU CUU GAU CAU CUU UUU UUC AAA UGC AUU UAU CGC UUC UUU AAA CAC	196
Ile Leu Asp His Leu Phe Phe Lys Cys Ile Tyr Arg Phe Phe Lys His	
45 50 55	
GGU CUG AAA AGA GGG CCU UCU ACG GAA GGA GUA CCA GAG UCU AUG AGG	244
Gly Leu Lys Arg Gly Pro Ser Thr Glu Gly Val Pro Glu Ser Met Arg	
60 65 70	
GAA GAA UAU CGA AAG GAA CAG CAG AGU GCU GUG GAU UCU GAC GAU AGU	292
Glu Glu Tyr Arg Lys Glu Gln Gln Ser Ala Val Asp Ser Asp Asp Ser	
75 80 85	
CAU UUU GUC AGC AUA GAG CUG GAG UAAAAAACUA CCUUGUUUCU ACU	339
His Phe Val Ser Ile Glu Leu Glu	
90 95	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly
1 5 10 15

Cys Arg Cys Asn Asp Ser Ser Asp Pro Leu Val Val Ala Ala Ser Ile
20 25 30

Ile Gly Ile Leu His Leu Ile Leu Trp Ile Leu Asp His Leu Phe Phe
35 40 45

Lys Cys Ile Tyr Arg Phe Phe Lys His Gly Leu Lys Arg Gly Pro Ser
50 55 60

Thr Glu Gly Val Pro Glu Ser Met Arg Glu Glu Tyr Arg Lys Glu Gln
65 70 75 80

Gln Ser Ala Val Asp Ser Asp Asp Ser His Phe Val Ser Ile Glu Leu
85 90 95

Glu

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: NP

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(113, "c")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain; a in wt2(3); a in 1988 reported ca vaccine strain (manuscript), but c reported in 1988 genbank"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(146, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(627, "c")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain and in wt2(3); a in 1988 reported ca vaccine strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(909, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); c in 1988 reported ca vaccine strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1550, "a")
- (D) OTHER INFORMATION: /note= "a in ca "master" strain and in wt2(3)"

/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 46..1539
- (D) OTHER INFORMATION: /product= "Nucleoprotein"
/gene= "NP"
/note= "nucleoprotein"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R W
- (B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) influenza virus
- (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
- (G) DATE: 1993
- (K) RELEVANT RESIDUES IN SEQ ID NO:9: FROM 1 TO 1566

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C
- (B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza vaccine strain, A/Ann Arbor/6/60 (H2N2)
- (C) JOURNAL: Virology
- (D) VOLUME: 167
- (F) PAGES: 554-567
- (G) DATE: 1988
- (K) RELEVANT RESIDUES IN SEQ ID NO:9: FROM 1 TO 1566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGCAAAAGCA GGGUAGAUAA UCACUCACUG AGUGACAUCA AAAUC AUG GCG UCC Met Ala Ser	54
1	
CAA GGC ACC AAA CGG UCU UAU GAA CAG AUG GAA ACU GAU GGG GAA CGC Gln Gly Thr Lys Arg Ser Tyr Glu Gln Met Glu Thr Asp Gly Glu Arg 5 10 15	102
CAG AAU GCA ACU GAA AUC AGA GCA UCC GUC GGG AAG AUG AUU GGU GGA Gln Asn Ala Thr Glu Ile Arg Ala Ser Val Gly Lys Met Ile Gly Gly 20 25 30 35	150
AUU GGA CGA UUC UAC AUC CAA AUG UGC ACC GAA CUU AAA CUC AGU GAU Ile Gly Arg Phe Tyr Ile Gln Met Cys Thr Glu Leu Lys Leu Ser Asp 40 45 50	198
UAU GAG GGG CGG CUG AUC CAG AAC AGC UUA ACA AUA GAG AGA AUG GUG Tyr Glu Gly Arg Leu Ile Gln Asn Ser Leu Thr Ile Glu Arg Met Val 55 60 65	246
CUC UCU GCU UUU GAC GAG AGG AGG AAU AAA UAU CUG GAA GAA CAU CCC Leu Ser Ala Phe Asp Glu Arg Arg Asn Lys Tyr Leu Glu Glu His Pro 70 75 80	294
AGC GCG GGG AAG GAU CCU AAG AAA ACU GGA GGA CCC AUA UAC AAG AGA Ser Ala Gly Lys Asp Pro Lys Lys Thr Gly Gly Pro Ile Tyr Lys Arg 85 90 95	342
GUA GAU GGA AAG UGG AUG AGG GAA CUC GUC CUU UAU GAC AAA GAA GAA Val Asp Gly Lys Trp Met Arg Glu Leu Val Leu Tyr Asp Lys Glu Glu 100 105 110 115	390
AUA AGG CGA AUC UGG CGC CAA GCU AAU AAU GGU GAU GAU GCA ACA GCU Ile Arg Arg Ile Trp Arg Gln Ala Asn Asn Gly Asp Asp Ala Thr Ala 120 125 130	438
GGU CUG ACU CAC AUG AUG AUC UGG CAU UCC AAU UUG AAU GAU ACA ACA Gly Leu Thr His Met Met Ile Trp His Ser Asn Leu Asn Asp Thr Thr 135 140 145	486
UAC CAG AGG ACA AGA GCU CUU GUU CGC ACC GGA AUG GAU CCC AGG AUG Tyr Gln Arg Thr Arg Ala Leu Val Arg Thr Gly Met Asp Pro Arg Met 150 155 160	534
UGC UCU UUG AUG CAG GGU UCG ACU CUC CCU AGG AGG UCU GGA GCC GCA Cys Ser Leu Met Gln Gly Ser Thr Leu Pro Arg Arg Ser Gly Ala Ala 165 170 175	582
GGC GCU GCA GUC AAA GGA GUU GGG ACA AUG GUG AUG GAG UUG AUC AGG Gly Ala Ala Val Lys Gly Val Gly Thr Met Val Met Glu Leu Ile Arg 180 185 190 195	630

AUG AUC AAA CGU GGG AUC AAU GAU CGG AAC UUC UGG AGA GGU GAG AAU Met Ile Lys Arg Gly Ile Asn Asp Arg Asn Phe Trp Arg Gly Glu Asn 200 205 210	678
Gly Arg Lys Thr Arg Asn Ala Tyr Glu Arg Met Cys Asn Ile Leu Lys 215 220 225	726
GGA AAA UUU CAA ACA GCU GCA CAA AGA GCA AUG AUG GAU CAA GUG AGA Gly Lys Phe Gln Thr Ala Ala Gln Arg Ala Met Met Asp Gln Val Arg 230 235 240	774
GAA AGC CGG AAC CCA GGA AAU GCU GAG AUC GAA GAU CUC AUC UUU CUG Glu Ser Arg Asn Pro Gly Asn Ala Glu Ile Glu Asp Leu Ile Phe Leu 245 250 255	822
GCA CGG UCU GCA CUC AUA UUG AGA GGG UCA GUU GCU CAC AAA UCU UGU Ala Arg Ser Ala Leu Ile Leu Arg Gly Ser Val Ala His Lys Ser Cys 260 265 270 275	870
CUG CCU GCC UGU GUG UAU GGA CCU GCC GUA GCC AGU GGG UAC GAC UUC Leu Pro Ala Cys Val Tyr Gly Pro Ala Val Ala Ser Gly Tyr Asp Phe 280 285 290	918
GAA AAA GAG GGA UAC UCU UUA GUA GGG AUA GAC CCU UUC AAA CUG CUU Glu Lys Glu Gly Tyr Ser Leu Val Gly Ile Asp Pro Phe Lys Leu Leu 295 300 305	966
CAA AAC AGC CAA GUA UAC AGC CUA AUC AGA CCG AAU GAG AAU CCA GCA Gln Asn Ser Gln Val Tyr Ser Leu Ile Arg Pro Asn Glu Asn Pro Ala 310 315 320	1014
CAC AAG AGU CAG CUG GUG UGG AUG GCA UGC AAU UCU GCU GCA UUU GAA His Lys Ser Gln Leu Val Trp Met Ala Cys Asn Ser Ala Ala Phe Glu 325 330 335	1062
GAU CUA AGA GUA UCA AGC UUC AUC AGA GGG ACC AAA GUA AUC CCA AGG Asp Leu Arg Val Ser Ser Phe Ile Arg Gly Thr Lys Val Ile Pro Arg 340 345 350 355	1110
GGG AAA CUU UCC ACU AGA GGA GUA CAA AUU GCU UCA AAU GAA AAC AUG Gly Lys Leu Ser Thr Arg Gly Val Gln Ile Ala Ser Asn Glu Asn Met 360 365 370	1158
GAU ACU AUG GGA UCA AGU ACU CUU GAA CUG AGA AGC AGG UAC UGG GCC Asp Thr Met Gly Ser Ser Thr Leu Glu Leu Arg Ser Arg Tyr Trp Ala 375 380 385	1206
AUA AGG ACC AGA AGU GGA GGA AAC ACU AAU CAA CAG AGG GCC UCU GCA Ile Arg Thr Arg Ser Gly Gly Asn Thr Asn Gln Gln Arg Ala Ser Ala 390 395 400	1254
GGU CAA AUC AGU GUA CAA CCU ACG UUU UCU GUG CAA AGA AAC CUC CCA Gly Gln Ile Ser Val Gln Pro Thr Phe Ser Val Gln Arg Asn Leu Pro 405 410 415	1302

Al
UUU GAC AAA CCA ACC AUC AUG GCA GCA UUC ACU GGG AAU GCA GAG GGA 1350
Phe Asp Lys Pro Thr Ile Met Ala Ala Phe Thr Gly Asn Ala Glu Gly
420 425 430 435
AGA ACA UCA GAC AUG AGG GCA GAA AUC AUA AGG AUG AUG GAA GGU GCA 1398
Arg Thr Ser Asp Met Arg Ala Glu Ile Ile Arg Met Met Glu Gly Ala
440 445 450
AAA CCA GAA GAA GUG UCC UUC CAG GGG CGG GGA GUC UUC GAG CUC UCG 1446
Lys Pro Glu Glu Val Ser Phe Gln Gly Arg Gly Val Phe Glu Leu Ser
455 460 465
GAC GAA AAG GCA ACG AAC CCG AUC GUG CCC UCU UUU GAC AUG AGU AAU 1494
Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp Met Ser Asn
470 475 480
GAA GGA UCU UAU UUC UUC GGA GAC AAU GCA GAG GAG UAC GAC AAU 1539
Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr Asp Asn
485 490 495
UAAGGAAAAA AUACCUUGU UUCUACU 1566

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Ser Gln Gly Thr Lys Arg Ser Tyr Glu Gln Met Glu Thr Asp
1 5 10 15
Gly Glu Arg Gln Asn Ala Thr Glu Ile Arg Ala Ser Val Gly Lys Met
20 25 30
Ile Gly Gly Ile Gly Arg Phe Tyr Ile Gln Met Cys Thr Glu Leu Lys
35 40 45
Leu Ser Asp Tyr Glu Gly Arg Leu Ile Gln Asn Ser Leu Thr Ile Glu
50 55 60
Arg Met Val Leu Ser Ala Phe Asp Glu Arg Arg Asn Lys Tyr Leu Glu
65 70 75 80
Glu His Pro Ser Ala Gly Lys Asp Pro Lys Lys Thr Gly Gly Pro Ile

85 90 95
A1
Tyr Lys Arg Val Asp Gly Lys Trp Met Arg Glu Leu Val Leu Tyr Asp
100 105 110
Lys Glu Glu Ile Arg Arg Ile Trp Arg Gln Ala Asn Asn Gly Asp Asp
115 120 125
Ala Thr Ala Gly Leu Thr His Met Met Ile Trp His Ser Asn Leu Asn
130 135 140
Asp Thr Thr Tyr Gln Arg Thr Arg Ala Leu Val Arg Thr Gly Met Asp
145 150 155 160
Pro Arg Met Cys Ser Leu Met Gln Gly Ser Thr Leu Pro Arg Arg Ser
165 170 175
Gly Ala Ala Gly Ala Ala Val Lys Gly Val Gly Thr Met Val Met Glu
180 185 190
Leu Ile Arg Met Ile Lys Arg Gly Ile Asn Asp Arg Asn Phe Trp Arg
195 200 205
Gly Glu Asn Gly Arg Lys Thr Arg Asn Ala Tyr Glu Arg Met Cys Asn
210 215 220
Ile Leu Lys Gly Lys Phe Gln Thr Ala Ala Gln Arg Ala Met Met Asp
225 230 235 240
Gln Val Arg Glu Ser Arg Asn Pro Gly Asn Ala Glu Ile Glu Asp Leu
245 250 255
Ile Phe Leu Ala Arg Ser Ala Leu Ile Leu Arg Gly Ser Val Ala His
260 265 270
Lys Ser Cys Leu Pro Ala Cys Val Tyr Gly Pro Ala Val Ala Ser Gly
275 280 285
Tyr Asp Phe Glu Lys Glu Gly Tyr Ser Leu Val Gly Ile Asp Pro Phe
290 295 300
Lys Leu Leu Gln Asn Ser Gln Val Tyr Ser Leu Ile Arg Pro Asn Glu
305 310 315 320
Asn Pro Ala His Lys Ser Gln Leu Val Trp Met Ala Cys Asn Ser Ala
325 330 335
Ala Phe Glu Asp Leu Arg Val Ser Ser Phe Ile Arg Gly Thr Lys Val
340 345 350
Ile Pro Arg Gly Lys Leu Ser Thr Arg Gly Val Gln Ile Ala Ser Asn
355 360 365
Glu Asn Met Asp Thr Met Gly Ser Ser Thr Leu Glu Leu Arg Ser Arg
370 375 380

A
Tyr Trp Ala Ile Arg Thr Arg Ser Gly Gly Asn Thr Asn Gln Gln Arg
385 390 395 400
Ala Ser Ala Gly Gln Ile Ser Val Gln Pro Thr Phe Ser Val Gln Arg
405 410 415
Asn Leu Pro Phe Asp Lys Pro Thr Ile Met Ala Ala Phe Thr Gly Asn
420 425 430
Ala Glu Gly Arg Thr Ser Asp Met Arg Ala Glu Ile Ile Arg Met Met
435 440 445
Glu Gly Ala Lys Pro Glu Glu Val Ser Phe Gln Gly Arg Gly Val Phe
450 455 460
Glu Leu Ser Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp
465 470 475 480
Met Ser Asn Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr
485 490 495

Asp Asn

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

(B) CLONE: PA

(ix) FEATURE:

(A) NAME/KEY: conflict

- (B) LOCATION: replace(20, "c")
(D) OTHER INFORMATION: /note= "c in ca "master" strain and in
wt2(3)"
/citation= ([1] [2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
(B) LOCATION: replace(75, "g")
(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); u in 1988 reported ca vaccine
strain"
/citation= ([1] [2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
(B) LOCATION: replace(1861, "g")
(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1] [2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
(B) LOCATION: replace(2167..2168, "cc")
(D) OTHER INFORMATION: /note= "cc in ca "master" strain and in
wt2(3)"
/citation= ([1] [2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 25..2172
(D) OTHER INFORMATION: /product= "polymerase acidic protein"
/gene= "PA"
/note= "polymerase acidic protein"
/citation= ([1] [2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:11: FROM 1 TO 2233

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza strain, A/Ann Arbor/6/60(H2N2)

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:11: FROM 1 TO 2233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCGAAAGCA GGUACUGAUC CGAA AUG GAA GAU UUU GUG CGA CAA UGC UUC Met Glu Asp Phe Val Arg Gln Cys Phe	51
1 5	
AAU CCG AUG AUU GUC GAG CUU GCG GAA AAA GCA AUG AAA GAG UAU GGA Asn Pro Met Ile Val Glu Leu Ala Glu Lys Ala Met Lys Glu Tyr Gly	99
10 15 20 25	
GAG GAU CUG AAA AUC GAA ACA AAC AAA UUU GCA GCA AUA UGC ACU CAC Glu Asp Leu Lys Ile Glu Thr Asn Lys Phe Ala Ala Ile Cys Thr His	147
30 35 40	
UUG GAA GUA UGC UUC AUG UAU UCA GAU UUU CAU UUC AUC AAU GAG CAA Leu Glu Val Cys Phe Met Tyr Ser Asp Phe His Phe Ile Asn Glu Gln	195
45 50 55	

GGC GAG UCA AUA AUA GUA GAG CUU GAU GAU CCA AAU GCA CUU UUG AAG Gly Glu Ser Ile Ile Val Glu Leu Asp Asp Pro Asn Ala Leu Leu Lys 60 65 70	243
CAC AGA UUU GAA AUA AUA GAG GGA AGA GAU CGC ACA AUG GCC UGG ACA His Arg Phe Glu Ile Ile Glu Gly Arg Asp Arg Thr Met Ala Trp Thr 75 80 85	291
GUA GUA AAC AGU AUU UGC AAC ACU ACA GGA GCU GAG AAA CCG AAG UUU Val Val Asn Ser Ile Cys Asn Thr Thr Gly Ala Glu Lys Pro Lys Phe 90 95 100 105	339
CUG CCA GAU UUG UAU GAU UAC AAG GAG AAU AGA UUC AUC GAG AUU GGA Leu Pro Asp Leu Tyr Asp Tyr Lys Glu Asn Arg Phe Ile Glu Ile Gly 110 115 120	387
GUG ACA AGG AGG GAA GUC CAC AUA UAC UAU CUU GAA AAG GCC AAU AAA Val Thr Arg Arg Glu Val His Ile Tyr Tyr Leu Glu Lys Ala Asn Lys 125 130 135	435
AUU AAA UCU GAG AAG ACA CAC AUC CAC AUU UUC UCA UUC ACU GGG GAA Ile Lys Ser Glu Lys Thr His Ile His Ile Phe Ser Phe Thr Gly Glu 140 145 150	483
GAA AUG GCC ACA AAG GCC GAC UAC ACU CUC GAU GAG GAA AGC AGG GCU Glu Met Ala Thr Lys Ala Asp Tyr Thr Leu Asp Glu Glu Ser Arg Ala 155 160 165	531
AGG AUC AAA ACC AGA CUA UUC ACC AUA AGA CAA GAA AUG GCU AGC AGA Arg Ile Lys Thr Arg Leu Phe Thr Ile Arg Gln Glu Met Ala Ser Arg 170 175 180 185	579
GGC CUC UGG GAU UCC UUU CAU CAG UCC GAA AGA GGC GAA GAA ACA AUU Gly Leu Trp Asp Ser Phe His Gln Ser Glu Arg Gly Glu Glu Thr Ile 190 195 200	627
GAA GAA AGA UUU GAA AUC ACA GGG ACA AUG CGC AGG CUC GCC GAC CAA Glu Glu Arg Phe Glu Ile Thr Gly Thr Met Arg Arg Leu Ala Asp Gln 205 210 215	675
AGU CUC CCG CCG AAC UUC UCC UGC CUU GAG AAU UUU AGA GCC UAU GUG Ser Leu Pro Pro Asn Phe Ser Cys Leu Glu Asn Phe Arg Ala Tyr Val 220 225 230	723
GAU GGA UUC GAA CCG AAC GGC UAC AUU GAG GGC AAG CUU UCU CAA AUG Asp Gly Phe Glu Pro Asn Gly Tyr Ile Glu Gly Lys Leu Ser Gln Met 235 240 245	771
UCC AAA GAA GUA AAU GCU AAA AUU GAA CCU UUU CUG AAA ACA ACA CCA Ser Lys Glu Val Asn Ala Lys Ile Glu Pro Phe Leu Lys Thr Thr Pro 250 255 260 265	819
AGA CCA AUU AGA CUU CCG GAU GGG CCU CCU UGU UCU CAG CGG UCC AAA Arg Pro Ile Arg Leu Pro Asp Gly Pro Pro Cys Ser Gln Arg Ser Lys 270 275 280	867

a'	UUC CUG CUG AUG GAU GCU UUA AAA UUA AGC AUU GAG GAC CCA AGU CAC Phe Leu Leu Met Asp Ala Leu Lys Leu Ser Ile Glu Asp Pro Ser His 285 290 295	915
	GAA GGA GAG GGA AUA CCA CUA UAU GAU GCG AUC AAG UGU AUG AGA ACA Glu Gly Glu Gly Ile Pro Leu Tyr Asp Ala Ile Lys Cys Met Arg Thr 300 305 310	963
	UUC UUU GGA UGG AAA GAA CCC UAU GUU GUU AAA CCA CAC GAA AAG GGA Phe Phe Gly Trp Lys Glu Pro Tyr Val Val Lys Pro His Glu Lys Gly 315 320 325	1011
	AUA AAU CCA AAU UAU CUG CUG UCA UGG AAG CAA GUA CUG GCA GAA CUG Ile Asn Pro Asn Tyr Leu Leu Ser Trp Lys Gln Val Leu Ala Glu Leu 330 335 340 345	1059
	CAG GAC AUU GAG AAU GAG GAG AAG AUU CCA AGA ACC AAA AAC AUG AAG Gln Asp Ile Glu Asn Glu Glu Lys Ile Pro Arg Thr Lys Asn Met Lys 350 355 360	1107
	AAA ACG AGU CAG CUA AAG UGG GCA CUU GGU GAG AAC AUG GCA CCA GAG Lys Thr Ser Gln Leu Lys Trp Ala Leu Gly Glu Asn Met Ala Pro Glu 365 370 375	1155
	AAG GUA GAC UUU GAC GAC UGU AGA GAU GUA AGC GAU UUG AAG CAA UAU Lys Val Asp Phe Asp Asp Cys Arg Asp Val Ser Asp Leu Lys Gln Tyr 380 385 390	1203
	GAU AGU GAU GAA CCU GAA UUA AGG UCA CUU UCA AGC UGG AUC CAG AAU Asp Ser Asp Glu Pro Glu Leu Arg Ser Leu Ser Ser Trp Ile Gln Asn 395 400 405	1251
	GAG UUC AAC AAG GCA UGC GAG CUG ACC GAU UCA AUC UGG AUA GAG CUC Glu Phe Asn Lys Ala Cys Glu Leu Thr Asp Ser Ile Trp Ile Glu Leu 410 415 420 425	1299
	GAU GAG AUU GGA GAA GAU GUG GCU CCA AUU GAA CAC AUU GCA AGC AUG Asp Glu Ile Gly Glu Asp Val Ala Pro Ile Glu His Ile Ala Ser Met 430 435 440	1347
	AGA AGG AAU UAC UUC ACA GCA GAG GUG UCU CAU UGC AGA GCC ACA GAA Arg Arg Asn Tyr Phe Thr Ala Glu Val Ser His Cys Arg Ala Thr Glu 445 450 455	1395
	UAU AUA AUG AAG GGG GUA UAC AUU AAU ACU GCC UUG CUU AAU GCA UCC Tyr Ile Met Lys Gly Val Tyr Ile Asn Thr Ala Leu Leu Asn Ala Ser 460 465 470	1443
	UGU GCA GCA AUG GAC GAU UUC CAA CUA AUU CCC AUG AUA AGC AAA UGU Cys Ala Ala Met Asp Asp Phe Gln Leu Ile Pro Met Ile Ser Lys Cys 475 480 485	1491
	AGA ACU AAA GAG GGA AGG CGA AAG ACC AAU UUA UAU GGU UUC AUC AUA Arg Thr Lys Glu Gly Arg Arg Lys Thr Asn Leu Tyr Gly Phe Ile Ile 490 495 500 505	1539

AAA GGA AGA UCU CAC UUA AGG AAU GAC ACC GAC GUG GUA AAC UUU GUG Lys Gly Arg Ser His Leu Arg Asn Asp Thr Asp Val Val Asn Phe Val 510 515 520	1587
AGC AUG GAG UUU UCU CUC ACU GAC CCA AGA CUU GAG CCA CAC AAA UGG Ser Met Glu Phe Ser Leu Thr Asp Pro Arg Leu Glu Pro His Lys Trp 525 530 535	1635
GAG AAG UAC UGU GUU CUU GAG AUA GGA GAU AUG CUA CUA AGA AGU GCC Glu Lys Tyr Cys Val Leu Glu Ile Gly Asp Met Leu Leu Arg Ser Ala 540 545 550	1683
AUA GGC CAG GUG UCA AGG CCC AUG UUC UUG UAU GUG AGG ACA AAU GGA Ile Gly Gln Val Ser Arg Pro Met Phe Leu Tyr Val Arg Thr Asn Gly 555 560 565	1731
ACA UCA AAG AUU AAA AUG AAA UGG GGA AUG GAG AUG AGG CGU UGC CUC Thr Ser Lys Ile Lys Met Lys Trp Gly Met Glu Met Arg Arg Cys Leu 570 575 580 585	1779
CUU CAG UCA CUC CAA CAA AUC GAG AGU AUG AUU GAA GCC GAG UCC UCU Leu Gln Ser Leu Gln Gln Ile Glu Ser Met Ile Glu Ala Glu Ser Ser 590 595 600	1827
GUC AAG GAG AAA GAC AUG ACC AAA GAG UUU UUC GAG AAU AAA UCA GAA Val Lys Glu Lys Asp Met Thr Lys Glu Phe Phe Glu Asn Lys Ser Glu 605 610 615	1875
ACA UGG CCC AUU GGA GAG UCC CCC AAA GGA GUG GAA GAA GGU UCC AUU Thr Trp Pro Ile Gly Glu Ser Pro Lys Gly Val Glu Glu Gly Ser Ile 620 625 630	1923
GGG AAG GUC UGC AGG ACU UUA UUA GCC AAG UCG GUA UUC AAU AGC CUG Gly Lys Val Cys Arg Thr Leu Leu Ala Lys Ser Val Phe Asn Ser Leu 635 640 645	1971
UAU GCA UCU CCA CAA UUA GAA GGA UUU UCA GCU GAA UCA AGA AAA CUG Tyr Ala Ser Pro Gln Leu Glu Gly Phe Ser Ala Glu Ser Arg Lys Leu 650 655 660 665	2019
CUU CUU GUC GUU CAG GCU CUU AGG GAC AAU CUU GAA CCU GGG ACC UUU Leu Leu Val Val Gln Ala Leu Arg Asp Asn Leu Glu Pro Gly Thr Phe 670 675 680	2067
GAU CUU GGG GGG CUA UAU GAA GCA AUU GAG GAG UGC CUG AUU AAU GAU Asp Leu Gly Gly Leu Tyr Glu Ala Ile Glu Glu Cys Leu Ile Asn Asp 685 690 695	2115
CCC UGG GUU UUG CUU AAU GCG UCU UGG UUC AAC UCC UUC CUA ACA CAU Pro Trp Val Leu Leu Asn Ala Ser Trp Phe Asn Ser Phe Leu Thr His 700 705 710	2163
GCA CCA AGA UAGUUGUGGC AAUGCACUA UUUGCACAU AUACUGUCCA Ala Pro Arg 715	2212

a/ AAAAGUACC UUGUUUCUAC U

2233

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Glu Asp Phe Val Arg Gln Cys Phe Asn Pro Met Ile Val Glu Leu
1 5 10 15

Ala Glu Lys Ala Met Lys Glu Tyr Gly Glu Asp Leu Lys Ile Glu Thr
20 25 30

Asn Lys Phe Ala Ala Ile Cys Thr His Leu Glu Val Cys Phe Met Tyr
35 40 45

Ser Asp Phe His Phe Ile Asn Glu Gln Gly Glu Ser Ile Ile Val Glu
50 55 60

Leu Asp Asp Pro Asn Ala Leu Leu Lys His Arg Phe Glu Ile Ile Glu
65 70 75 80

Gly Arg Asp Arg Thr Met Ala Trp Thr Val Val Asn Ser Ile Cys Asn
85 90 95

Thr Thr Gly Ala Glu Lys Pro Lys Phe Leu Pro Asp Leu Tyr Asp Tyr
100 105 110

Lys Glu Asn Arg Phe Ile Glu Ile Gly Val Thr Arg Arg Glu Val His
115 120 125

Ile Tyr Tyr Leu Glu Lys Ala Asn Lys Ile Lys Ser Glu Lys Thr His
130 135 140

Ile His Ile Phe Ser Phe Thr Gly Glu Met Ala Thr Lys Ala Asp
145 150 155 160

Tyr Thr Leu Asp Glu Glu Ser Arg Ala Arg Ile Lys Thr Arg Leu Phe
165 170 175

Thr Ile Arg Gln Glu Met Ala Ser Arg Gly Leu Trp Asp Ser Phe His
180 185 190

Gln Ser Glu Arg Gly Glu Glu Thr Ile Glu Glu Arg Phe Glu Ile Thr
195 200 205

Gly Thr Met Arg Arg Leu Ala Asp Gln Ser Leu Pro Pro Asn Phe Ser
210 215 220

Cys Leu Glu Asn Phe Arg Ala Tyr Val Asp Gly Phe Glu Pro Asn Gly
225 230 235 240

Tyr Ile Glu Gly Lys Leu Ser Gln Met Ser Lys Glu Val Asn Ala Lys
245 250 255

Ile Glu Pro Phe Leu Lys Thr Thr Pro Arg Pro Ile Arg Leu Pro Asp
260 265 270

Gly Pro Pro Cys Ser Gln Arg Ser Lys Phe Leu Leu Met Asp Ala Leu
275 280 285

Lys Leu Ser Ile Glu Asp Pro Ser His Glu Gly Glu Gly Ile Pro Leu
290 295 300

Tyr Asp Ala Ile Lys Cys Met Arg Thr Phe Phe Gly Trp Lys Glu Pro
305 310 315 320

Tyr Val Val Lys Pro His Glu Lys Gly Ile Asn Pro Asn Tyr Leu Leu
325 330 335

Ser Trp Lys Gln Val Leu Ala Glu Leu Gln Asp Ile Glu Asn Glu Glu
340 345 350

Lys Ile Pro Arg Thr Lys Asn Met Lys Lys Thr Ser Gln Leu Lys Trp
355 360 365

Ala Leu Gly Glu Asn Met Ala Pro Glu Lys Val Asp Phe Asp Asp Cys
370 375 380

Arg Asp Val Ser Asp Leu Lys Gln Tyr Asp Ser Asp Glu Pro Glu Leu
385 390 395 400

Arg Ser Leu Ser Ser Trp Ile Gln Asn Glu Phe Asn Lys Ala Cys Glu
405 410 415

Leu Thr Asp Ser Ile Trp Ile Glu Leu Asp Glu Ile Gly Glu Asp Val
420 425 430

Ala Pro Ile Glu His Ile Ala Ser Met Arg Arg Asn Tyr Phe Thr Ala
435 440 445

Glu Val Ser His Cys Arg Ala Thr Glu Tyr Ile Met Lys Gly Val Tyr
450 455 460

Ile Asn Thr Ala Leu Leu Asn Ala Ser Cys Ala Ala Met Asp Asp Phe
465 470 475 480

Gln Leu Ile Pro Met Ile Ser Lys Cys Arg Thr Lys Glu Gly Arg Arg

485

490

495

Lys Thr Asn Leu Tyr Gly Phe Ile Ile Lys Gly Arg Ser His Leu Arg
500 505 510

Asn Asp Thr Asp Val Val Asn Phe Val Ser Met Glu Phe Ser Leu Thr
515 520 525

Asp Pro Arg Leu Glu Pro His Lys Trp Glu Lys Tyr Cys Val Leu Glu
530 535 540

Ile Gly Asp Met Leu Leu Arg Ser Ala Ile Gly Gln Val Ser Arg Pro
545 550 555 560

Met Phe Leu Tyr Val Arg Thr Asn Gly Thr Ser Lys Ile Lys Met Lys
565 570 575

Trp Gly Met Glu Met Arg Arg Cys Leu Leu Gln Ser Leu Gln Gln Ile
580 585 590

Glu Ser Met Ile Glu Ala Glu Ser Ser Val Lys Glu Lys Asp Met Thr
595 600 605

Lys Glu Phe Phe Glu Asn Lys Ser Glu Thr Trp Pro Ile Gly Glu Ser
610 615 620

Pro Lys Gly Val Glu Glu Gly Ser Ile Gly Lys Val Cys Arg Thr Leu
625 630 635 640

Leu Ala Lys Ser Val Phe Asn Ser Leu Tyr Ala Ser Pro Gln Leu Glu
645 650 655

Gly Phe Ser Ala Glu Ser Arg Lys Leu Leu Leu Val Val Gln Ala Leu
660 665 670

Arg Asp Asn Leu Glu Pro Gly Thr Phe Asp Leu Gly Gly Leu Tyr Glu
675 680 685

Ala Ile Glu Glu Cys Leu Ile Asn Asp Pro Trp Val Leu Leu Asn Ala
690 695 700

Ser Trp Phe Asn Ser Phe Leu Thr His Ala Pro Arg
705 710 715

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2341 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Influenza virus

(B) STRAIN: cold adapted "Master Strain" A/AA/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

(B) CLONE: PB1

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(123, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1] [2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(486, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3)"
/citation= ([1] [2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1195, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1] [2])

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(1276, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain; a in wt2(3); g in 1988 reported ca vaccine strain"
/citation= ([1][2])

ai
(ix) FEATURE:

(A) NAME/KEY: conflict
(B) LOCATION: replace(1395, "u")
(D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict
(B) LOCATION: replace(1766, "g")
(D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict
(B) LOCATION: replace(2005, "a")
(D) OTHER INFORMATION: /note= "a in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict
(B) LOCATION: replace(2019, "u")
(D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 25..2295

(D) OTHER INFORMATION: /product= "polymerase basic 1"
/gene= "PB1"
/note= "polymerase basic 1"
/citation= ([1][2])

al
(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:13: FROM 1 TO 2341

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza vaccine strain

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:13: FROM 1 TO 2341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCGAAAGCA GGCAAACCAU UUGA AUG GAU GUC AAU CCG ACC UUA CUU UUC Met Asp Val Asn Pro Thr Leu Leu Phe	51
1 5	

UUG AAA GUU CCA GCG CAA AAU GCC AUA AGU ACU ACA UUC CCU UAU ACU Leu Lys Val Pro Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr	99
10 15 20 25	

GGA	GAU	CCU	CCA	UAC	AGC	CAU	GGG	ACA	GGA	ACA	GGA	UAC	ACC	AUG	GAC		147
Gly	Asp	Pro	Pro	Tyr	Ser	His	Gly	Thr	Gly	Thr	Gly	Tyr	Thr	Met	Asp		
30							35							40			
<i>at</i>																	
ACA	GUC	AAC	AGA	ACA	CAU	CAA	UAU	UCA	GAA	AAG	GGG	AAG	UGG	ACA	ACA		195
Thr	Val	Asn	Arg	Thr	His	Gln	Tyr	Ser	Glu	Lys	Gly	Lys	Trp	Thr	Thr		
45							50						55				
AAC	ACG	GAA	ACU	GGA	GCG	CAC	CAA	CUU	AAC	CCA	AUU	GAU	GGA	CCA	CUA		243
Asn	Thr	Glu	Thr	Gly	Ala	His	Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu		
60							65						70				
CCU	GAG	GAC	AAU	GAA	CCA	AGU	GGA	UAU	GCA	CAA	ACA	GAC	UGC	GUC	CUG		291
Pro	Glu	Asp	Asn	Glu	Pro	Ser	Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu		
75							80						85				
GAA	GCA	AUG	GCU	UUC	CUU	GAA	GAA	UCC	CAC	CCA	GGA	AUC	UUU	GAA	AAC		339
Glu	Ala	Met	Ala	Phe	Leu	Glu	Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Asn		
90						95				100				105			
UCG	UGU	CUU	GAA	ACG	AUG	GAA	GUU	AUU	CAA	CAA	ACA	AGA	GUG	GAC	AAA		387
Ser	Cys	Leu	Glu	Thr	Met	Glu	Val	Ile	Gln	Gln	Thr	Arg	Val	Asp	Lys		
110						115							120				
CUG	ACC	CAA	GGU	CGU	CAG	ACC	UAU	GAU	UGG	ACA	UUG	AAC	AGA	AAU	CAG		435
Leu	Thr	Gln	Gly	Arg	Gln	Thr	Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln		
125						130							135				
CCG	GCU	GCA	ACU	GCG	CUA	GCC	AAC	ACU	AUA	GAG	GUC	UUC	AGA	UCG	AAU		483
Pro	Ala	Ala	Thr	Ala	Leu	Ala	Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn		
140						145							150				
GGU	CUG	ACA	GCU	AAU	GAA	UCG	GGA	AGG	CUA	AUA	GAU	UUC	CUC	AAG	GAU		531
Gly	Leu	Thr	Ala	Asn	Glu	Ser	Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp		
155						160							165				
GUG	AUA	GAA	UCA	AUG	GAU	AAA	GAG	GAG	AUG	GAA	AUC	ACA	ACA	CAC	UUC		579
Val	Ile	Glu	Ser	Met	Asp	Lys	Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe		
170						175					180			185			
CAA	AGA	AAA	AGA	AGA	GUU	AGA	GAC	AAC	AUG	ACC	AAG	AAA	AUG	GUC	ACA		627
Gln	Arg	Lys	Arg	Arg	Val	Arg	Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr		
190						195							200				
CAA	CGA	ACA	AUA	GGA	AAG	AAG	CAA	AGA	UUG	AAC	AAG	AGA	AGC	UAU		675	
Gln	Arg	Thr	Ile	Gly	Lys	Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr			
205						210							215				
CUA	AUA	AGA	GCA	CUG	ACA	UUG	AAC	ACA	AUG	ACU	AAA	GAU	GCA	GAG	AGA		723
Leu	Ile	Arg	Ala	Leu	Thr	Leu	Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg		
220						225							230				
GGU	AAA	UUU	AAG	AGA	AGA	GCA	AUU	GCA	ACA	CCC	GGU	AUG	CAG	AUC	AGA		771
Gly	Lys	Leu	Lys	Arg	Arg	Ala	Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg		
235						240							245				

GGG UUC GUG UAC UUU GUC GAA ACA CUA GCG AGA AGU AUU UGU GAG AAG Gly Phe Val Tyr Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys 250 255 260 265	819
CUU GAA CAG UCU GGG CUU CCG GUU GGA GGU AAU GAA AAG AAG GCU AAA Leu Glu Gln Ser Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys 270 275 280	867
CUG GCA AAU GUU GUG CGA AAA AUG AUG ACU AAU UCA CAA GAC ACA GAG Leu Ala Asn Val Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu 285 290 295	915
CUC UCU UUC ACA AUU ACU GGA GAC AAU ACC AAA UGG AAU GAG AAU CAA Leu Ser Phe Thr Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln 300 305 310	963
AAU CCU CGG AUG UUC CUG GCG AUG AUA ACA UAC AUC ACA AGA AAU CAA Asn Pro Arg Met Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln 315 320 325	1011
CCU GAA UGG UUU AGA AAC GUC CUG AGC AUC GCA CCU AUA AUG UUC UCA Pro Glu Trp Phe Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser 330 335 340 345	1059
AAU AAA AUG GCA AGA CUA GGG AAA GGA UAC AUG UUC AAA AGC AAG AGC Asn Lys Met Ala Arg Leu Gly Lys Gly Tyr Met Phe Lys Ser Lys Ser 350 355 360	1107
AUG AAG CUC CGA ACA CAA AUA CCA GCA GAA AUG CUA GCA AGU AUU GAC Met Lys Leu Arg Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp 365 370 375	1155
CUG AAA UAC UUU AAU GAA UCA ACA AGA AAG AAA AUC GAG GAA AUA AGG Leu Lys Tyr Phe Asn Glu Ser Thr Arg Lys Lys Ile Glu Glu Ile Arg 380 385 390	1203
CCU CUC CUA AUA GAU GGC ACA GUC UCA UUG AGU CCU GGA AUG AUG AUG Pro Leu Leu Ile Asp Gly Thr Val Ser Leu Ser Pro Gly Met Met Met 395 400 405	1251
GCG AUG UUC AAC AUG CUA AGU ACA GUC UUA GGA GUC UCA AUC CUG AAU Gly Met Phe Asn Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn 410 415 420 425	1299
CUU GGA CAA AAG AAG UAC ACC AAA ACA ACA UAC UGG UGG GAC GGA CUC Leu Gly Gln Lys Lys Tyr Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu 430 435 440	1347
CAA UCC UCU GAU GAC UUC GCC CUC AUA GUG AAU GCA CCA AAU CAU GAU Gln Ser Ser Asp Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Asp 445 450 455	1395
GGA AUA CAA GCA GGG GUG GAU AGA UUC UAC AGA ACC UGC AAG CUA GUC Gly Ile Gln Ala Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val 460 465 470	1443

GGA AUC AAU AUG AGC AAA AAG AAG UCC UAC AUA AAU AGG ACA GGG ACA Gly Ile Asn Met Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr 475 480 485	1491
UUU GAA UUC ACA AGC UUU UUC UAU CGC UAU GGA UUU GUA GCC AAU UUU Phe Glu Phe Thr Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe 490 495 500 505	1539
AGC AUG GAG CUG CCC AGC UUU GGA GUG UCU GGA AUU AAU GAA UCG GCU Ser Met Glu Leu Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala 510 515 520	1587
GAU AUG AGC AUU GGG GUA ACA GUG AUA AAG AAC AAC AUG AUA AAC AAU Asp Met Ser Ile Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn 525 530 535	1635
GAC CUU GGG CCA GCA ACA GCC CAA CUG GCU CUU CAA CUA UUC AUC AAA Asp Leu Gly Pro Ala Thr Ala Gln Leu Ala Leu Gln Leu Phe Ile Lys 540 545 550	1683
GAC UAC AGA UAU ACG UAC CGG UGC CAC AGA GGA GAC ACA CAA AUU CAG Asp Tyr Arg Tyr Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln 555 560 565	1731
ACA AGG AGA UCA UUC GAG CUA AAG AAG CUG UGG GGG CAA ACC CGC UCA Thr Arg Arg Ser Phe Glu Leu Lys Lys Leu Trp Gly Gln Thr Arg Ser 570 575 580 585	1779
AAG GCA GGA CUU UUG GUU UCG GAU GGA GGA CCA AAC UUA UAC AAU AUC Lys Ala Gly Leu Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile 590 595 600	1827
CGG AAU CUC CAC AUU CCA GAA GUC UGC UUG AAG UGG GAG CUA AUG GAU Arg Asn Leu His Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp 605 610 615	1875
GAA GAC UAU CAG GGG AGG CUU UGU AAU CCC CUG AAU CCA UUU GUC AGU Glu Asp Tyr Gln Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Ser 620 625 630	1923
CAU AAG GAG AUU GAG UCU GUA AAC AAU GCU GUG GUA AUG CCA GCU CAC His Lys Glu Ile Glu Ser Val Asn Asn Ala Val Val Met Pro Ala His 635 640 645	1971
GGU CCA GCC AAG AGC AUG GAA UAU GAU GCU GUU ACU ACU ACA CAC UCU Gly Pro Ala Lys Ser Met Glu Tyr Asp Ala Val Thr Thr Thr His Ser 650 655 660 665	2019
UGG AUC CCU AAG AGG AAC CGC UCC AUU CUC AAC ACA AGC CAA AGG GGA Trp Ile Pro Lys Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly 670 675 680	2067
AUU CUU GAA GAU GAA CAG AUG UAU CAG AAG UGU UGC AAU CUA UUC GAG Ile Leu Glu Asp Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu 685 690 695	2115

AAA UUC UUC CCU AGC AGU UCG UAC AGG AGA CCA GUU GGA AUU UCC AGC Lys Phe Phe Pro Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser 700 705 710	2163
AUG GUG GAG GCC AUG GUG UCU AGG GCC CGG AUU GAU GCA CGG AUU GAC Met Val Glu Ala Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp 715 720 725	2211
UUC GAG UCU GGA CGG AUU AAG AAA GAG GAG UUC GCU GAG AUC AUG AAG Phe Glu Ser Gly Arg Ile Lys Lys Glu Glu Ala Glu Ile Met Lys 730 735 740 745	2259
AUC UGU UCC ACC AUU GAA GAG CUC AGA CGG CAA AAA UAGUGAAUUU Ile Cys Ser Thr Ile Glu Glu Leu Arg Arg Gln Lys 750 755	2305
AGCUUGUCCU UCAUGAAAAA AUGCCUUGUU UCUACU	2341

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn
1 5 10 15

Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
20 25 30

Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
35 40 45

Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr Gly Ala His
50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
85 90 95

Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu Thr Met Glu

100	105	110
Val Ile Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr		
115	120	125
Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala		
130	135	140
Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser		
145	150	155
Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Ile Glu Ser Met Asp Lys		
165	170	175
Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg		
180	185	190
Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Lys		
195	200	205
Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu		
210	215	220
Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala		
225	230	235
Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu		
245	250	255
Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro		
260	265	270
Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys		
275	280	285
Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly		
290	295	300
Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala		
305	310	315
Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val		
325	330	335
Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly		
340	345	350
Lys Gly Tyr Met Phe Lys Ser Lys Ser Met Lys Leu Arg Thr Gln Ile		
355	360	365
Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Ser		
370	375	380
Thr Arg Lys Lys Ile Glu Glu Ile Arg Pro Leu Leu Ile Asp Gly Thr		
385	390	395
		400

Val Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
405 410 415

Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Lys Tyr Thr
420 425 430

Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
435 440 445

Leu Ile Val Asn Ala Pro Asn His Asp Gly Ile Gln Ala Gly Val Asp
450 455 460

Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
465 470 475 480

Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
485 490 495

Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
500 505 510

Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
515 520 525

Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
530 535 540

Gln Leu Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
545 550 555 560

Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
565 570 575

Lys Lys Leu Trp Gly Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
580 585 590

Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
595 600 605

Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
610 615 620

Cys Asn Pro Leu Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
625 630 635 640

Asn Asn Ala Val Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
645 650 655

Tyr Asp Ala Val Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser

690 695 700
Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
705 710 715 720
Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
725 730 735
Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
740 745 750
Leu Arg Arg Gln Lys
755

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PB2

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(141, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain; a in wt2(3); g in 1988 reported ca vaccine strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(426, "c")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(714, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3); c in 1988 reported ca vaccine strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(821, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(963, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); a in 1988 reported ca vaccine strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1182, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1212, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1353, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1923, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(1933, "c")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain; u in
wt2(3); u in 1988 reported ca vaccine
strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 28..2304
- (D) OTHER INFORMATION: /product= "polymerase basic 2"
/gene= "PB2"
/note= "polymerase basic 2"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
- (B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) influenza virus
- (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
- (G) DATE: 1993
- (K) RELEVANT RESIDUES IN SEQ ID NO:15: FROM 1 TO 2341

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C
- (B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza vaccine strain, A/Ann Arbor/6/60(H2N2)
- (C) JOURNAL: Virology
- (D) VOLUME: 167
- (F) PAGES: 554-567
- (G) DATE: 1988
- (K) RELEVANT RESIDUES IN SEQ ID NO:15: FROM 1 TO 2341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGCGAAAGCA GGUCAUUUAU AUUCAAU AUG GAA AGA AUA AAA GAA CUA CGG	51
Met Glu Arg Ile Lys Glu Leu Arg	
1 5	
AAU CUG AUG UCG CAG UCU CGC ACU CGC GAG AUA CUA ACA AAA ACC ACA	99
Asn Leu Met Ser Gln Ser Arg Thr Arg Glu Ile Leu Thr Lys Thr Thr	
10 15 20	
GUG GAC CAU AUG GCC AUA AUU AAG AAG UAC ACA UCA GGG AGG CAG GAA	147
Val Asp His Met Ala Ile Ile Lys Lys Tyr Thr Ser Gly Arg Gln Glu	
25 30 35 40	
AAG AAC CCG UCA CUU AGG AUG AAA UGG AUG AUG GCA AUG AAA UAU CCG	195

Lys Asn Pro Ser Leu Arg Met Lys Trp Met Met Ala Met Lys Tyr Pro		
45 50 55		
AUU ACA GCC GAC AAG AGG AUA ACA GAA AUG AUU CCU GAG AGA AAU GAG Ile Thr Ala Asp Lys Arg Ile Thr Glu Met Ile Pro Glu Arg Asn Glu	243	
60 65 70		
CAA GGG CAA ACU CUA UGG AGU AAA AUG AGU GAU GCC GGA UCG GAU CGU Gln Gly Gln Thr Leu Trp Ser Lys Met Ser Asp Ala Gly Ser Asp Arg	291	
75 80 85		
GUG AUG GUA UCA CCU CUG GCU GUG ACA UGG UGG AAU AGA AAU GGA CCA Val Met Val Ser Pro Leu Ala Val Thr Trp Trp Asn Arg Asn Gly Pro	339	
90 95 100		
AUG ACA AGU ACG GUU CAU UAU CCA AAA AUC UAC AAA ACU UAU UUU GAG Met Thr Ser Thr Val His Tyr Pro Lys Ile Tyr Lys Thr Tyr Phe Glu	387	
105 110 115 120		
AAA GUC GAA AGG UUA AAA CAU GGA ACC UUU GGC CCU GUC CAU UUU AGA Lys Val Glu Arg Leu Lys His Gly Thr Phe Gly Pro Val His Phe Arg	435	
125 130 135		
AAC CAA GUC AAA AUA CGC CGA AGA GUU GAC AUA AAU CCU GGU CAU GCA Asn Gln Val Lys Ile Arg Arg Val Asp Ile Asn Pro Gly His Ala	483	
140 145 150		
GAC CUC AGU GCC AAG GAG GCA CAG GAU GUA AUC AUG GAA GUU GUU UUC Asp Leu Ser Ala Lys Glu Ala Gln Asp Val Ile Met Glu Val Val Phe	531	
155 160 165		
CCU AAC GAA GUG GGG GCC AGG AUA CUA ACG UCG GAA UCG CAA UUA ACA Pro Asn Glu Val Gly Ala Arg Ile Leu Thr Ser Glu Ser Gln Leu Thr	579	
170 175 180		
AUA ACC AAA GAG AAA AAA GAA GAA CUC CAG GAU UGC AAA AUU UCA CCU Ile Thr Lys Glu Lys Glu Glu Leu Gln Asp Cys Lys Ile Ser Pro	627	
185 190 195 200		
UUG AUG GUU GCG UAC AUG UUA GAG AGA GAA CUU GUC CGA AAA ACG AGA Leu Met Val Ala Tyr Met Leu Glu Arg Glu Leu Val Arg Lys Thr Arg	675	
205 210 215		
UUU CUC CCA GUU GCU GGU GGA ACA AGC AGU GUG UAC AUU GAA GUG UUG Phe Leu Pro Val Ala Gly Gly Thr Ser Ser Val Tyr Ile Glu Val Leu	723	
220 225 230		
CAC UUG ACU CAA GGA ACA UGC UGG GAA CAG AUG UAC ACU CCA GGU GGA His Leu Thr Gln Gly Thr Cys Trp Glu Gln Met Tyr Thr Pro Gly Gly	771	
235 240 245		
GAA GUG AGG AAU GAU GAU GUU GAU CAA AGU CUA AUU AUU GCA GCC AGG Glu Val Arg Asn Asp Asp Val Asp Gln Ser Leu Ile Ile Ala Ala Arg	819	
250 255 260		

AGC AUA GUG AGA AGA GCA GCA GUA UCA GCA GAU CCA CUA GCA UCU UUA Ser Ile Val Arg Arg Ala Ala Val Ser Ala Asp Pro Leu Ala Ser Leu 265 270 275 280	867
UUG GAG AUG UGC CAC AGC ACA CAG AUU GGC GGG ACA AGG AUG GUG GAC Leu Glu Met Cys His Ser Thr Gln Ile Gly Gly Thr Arg Met Val Asp 285 290 . 295	915
AUU CUU AGG CAG AAC CCA ACA GAA GAG CAA GCU GUG GAA AUA UGC AAG Ile Leu Arg Gln Asn Pro Thr Glu Glu Gln Ala Val Glu Ile Cys Lys 300 305 310	963
GCU GCA AUG GGA CUG AGG AUC AGC UCA UCC UUC AGU UUU GGC GGG UUC Ala Ala Met Gly Leu Arg Ile Ser Ser Phe Ser Phe Gly Gly Phe 315 320 325	1011
ACA UUU AAG AGA ACA AGC GGA UCA UCA GUC AAG AGA GAG GAA GAA GUG Thr Phe Lys Arg Thr Ser Gly Ser Ser Val Lys Arg Glu Glu Glu Val 330 335 340	1059
CUU ACG GGC AAU CUU CAA ACA UUG AAA AUA AGG GUG CAU GAG GGA UAC Leu Thr Gly Asn Leu Gln Thr Leu Lys Ile Arg Val His Glu Gly Tyr 345 350 355 360	1107
GAG GAG UUC ACA AUG GUU GGG AAA AGG GCA ACA GCU AUA CUC AGA AAA Glu Glu Phe Thr Met Val Gly Lys Arg Ala Thr Ala Ile Leu Arg Lys 365 370 375	1155
GCA ACC AGG AGA UUG AUU CAG CUG AUU GUG AGU GGA AGA GAC GAA CAG Ala Thr Arg Arg Leu Ile Gln Leu Ile Val Ser Gly Arg Asp Glu Gln 380 385 390	1203
UCG AUA GCU GAA GCA AUA AUU GUG GCC AUG GUA UUU UCA CAA GAA GAU Ser Ile Ala Glu Ala Ile Ile Val Ala Met Val Phe Ser Gln Glu Asp 395 400 405	1251
UGU AUG AUA AAA GCA GUU AGA GGU GAU CUG AAU UUC GUU AAU AGG GCA Cys Met Ile Lys Ala Val Arg Gly Asp Leu Asn Phe Val Asn Arg Ala 410 415 420	1299
AAU CAG CGA UUG AAU CCC AUG CAU CAA CUU UUA AGA CAU UUU CAG AAG Asn Gln Arg Leu Asn Pro Met His Gln Leu Leu Arg His Phe Gln Lys 425 430 435 440	1347
GAU GCG AAA GUG CUU UUU CAA AAU UGG GGA AUU GAA CAU AUC GAC AAU Asp Ala Lys Val Leu Phe Gln Asn Trp Gly Ile Glu His Ile Asp Asn 445 450 455	1395
GUG AUG GGA AUG AUU GGG GUA UUA CCA GAC AUG ACU CCA AGC ACA GAG Val Met Gly Met Ile Gly Val Leu Pro Asp Met Thr Pro Ser Thr Glu 460 465 470	1443
AUG UCA AUG AGA GGG GUA AGA GUC AGC AAA AUG GGC GUA GAU GAA UAC Met Ser Met Arg Gly Val Arg Val Ser Lys Met Gly Val Asp Glu Tyr 475 480 485	1491

UCC AGC GCG GAG AGA GUA GUG GUG AGC AUU GAC CGG UUU UUG AGA GUU Ser Ser Ala Glu Arg Val Val Val Ser Ile Asp Arg Phe Leu Arg Val 490 495 500	1539
CGA GAC CAA CGA GGA AAU GUA CUA CUA UCU CCU GAG GAG GUC AGU GAA Arg Asp Gln Arg Gly Asn Val Leu Leu Ser Pro Glu Glu Val Ser Glu 505 510 515 520	1587
ACA CAG GGA ACA GAG AAA CUG ACA AUA ACU UAC UCA UCG UCA AUG AUG Thr Gln Gly Thr Glu Lys Leu Thr Ile Thr Tyr Ser Ser Ser Met Met 525 530 535	1635
UGG GAG AUU AAU GGC CCU GAG UCA GUG UUG GUC AAU ACC UAU CAG UGG Trp Glu Ile Asn Gly Pro Glu Ser Val Leu Val Asn Thr Tyr Gln Trp 540 545 550	1683
AUC AUC AGA AAC UGG GAA ACU GUU AAA AUU CAG UGG UCU CAG AAU CCU Ile Ile Arg Asn Trp Glu Thr Val Lys Ile Gln Trp Ser Gln Asn Pro 555 560 565	1731
ACA AUG CUA UAC AAU AAA AUG GAA UUU GAG CCA UUU CAG UCU UUA GUU Thr Met Leu Tyr Asn Lys Met Glu Phe Glu Pro Phe Gln Ser Leu Val 570 575 580	1779
CCU AAG GCC AUU AGA GGC CAA UAC AGU GGG UUU GUU AGG ACU CUA UUC Pro Lys Ala Ile Arg Gly Gln Tyr Ser Gly Phe Val Arg Thr Leu Phe 585 590 595 600	1827
CAA CAA AUG AGG GAU GUA CUU GGG ACA UUU GAU ACC ACC CAG AUA AUA Gln Gln Met Arg Asp Val Leu Gly Thr Phe Asp Thr Thr Gln Ile Ile 605 610 615	1875
AAA CUU CUU CCC UUU GCA GCC GCC CCA CCA AAG CAA AGU AGA AUG CAG Lys Leu Leu Pro Phe Ala Ala Ala Pro Pro Lys Gln Ser Arg Met Gln 620 625 630	1923
UUC UCU UCA CUG ACU GUG AAU GUG AGG GGA UCA GGA AUG AGA AUA CUU Phe Ser Ser Leu Thr Val Asn Val Arg Gly Ser Gly Met Arg Ile Leu 635 640 645	1971
GUA AGG GGC AAU UCU CCU AUA UUC AAC UAC AAC AAG ACC ACU AAG AGA Val Arg Gly Asn Ser Pro Ile Phe Asn Tyr Asn Lys Thr Thr Lys Arg 650 655 660	2019
CUA ACA AUU CUC GGA AAG GAU GCU GGC ACU UUA ACU GAA GAC CCA GAU Leu Thr Ile Leu Gly Lys Asp Ala Gly Thr Leu Thr Glu Asp Pro Asp 665 670 675 680	2067
GAA GGC ACA UCU GGA GUG GAG UCC GCU GUU CUG AGA GGA UUC CUC AUU Glu Gly Thr Ser Gly Val Glu Ser Ala Val Leu Arg Gly Phe Leu Ile 685 690 695	2115
CUG GGC AAA GAA GAU AGG AGA UAU GGA CCA GCA UUA AGC AUC AAU GAA Leu Gly Lys Glu Asp Arg Arg Tyr Gly Pro Ala Leu Ser Ile Asn Glu 700 705 710	2163

CUG AGU AAC CUU GCG AAA GGA GAA AAG GCU AAU GUA CUA AUU GGG CAA 2211
Leu Ser Asn Leu Ala Lys Gly Glu Lys Ala Asn Val Leu Ile Gly Gln
715 720 725

Gly Asp Val Val Leu Val Met Lys Arg Lys Arg Asn Ser Ser Ile Leu 2259
730 735 740

ACU GAC AGC CAG ACA GCG ACC AAA AGG AUU CGG AUG GCC AUC AAU 2304
Thr Asp Ser Gln Thr Ala Thr Lys Arg Ile Arg Met Ala Ile Asn
745 750 755

UAAUGUUGAA UAGUUUAAAA ACGACCUUGU UUCUACU 2341

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 759 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Glu Arg Ile Lys Glu Leu Arg Asn Leu Met Ser Gln Ser Arg Thr
1 5 10 15

Arg Glu Ile Leu Thr Lys Thr Val Asp His Met Ala Ile Ile Lys
20 25 30

Lys Tyr Thr Ser Gly Arg Gln Glu Lys Asn Pro Ser Leu Arg Met Lys
35 40 45

Trp Met Met Ala Met Lys Tyr Pro Ile Thr Ala Asp Lys Arg Ile Thr
50 55 60

Glu Met Ile Pro Glu Arg Asn Glu Gln Gly Gln Thr Leu Trp Ser Lys
65 70 75 80

Met Ser Asp Ala Gly Ser Asp Arg Val Met Val Ser Pro Leu Ala Val
85 90 95

Thr Trp Trp Asn Arg Asn Gly Pro Met Thr Ser Thr Val His Tyr Pro
100 105 110

Lys Ile Tyr Lys Thr Tyr Phe Glu Lys Val Glu Arg Leu Lys His Gly
115 120 125

Thr Phe Gly Pro Val His Phe Arg Asn Gln Val Lys Ile Arg Arg Arg
130 135 140

Val Asp Ile Asn Pro Gly His Ala Asp Leu Ser Ala Lys Glu Ala Gln
145 150 155 160

Asp Val Ile Met Glu Val Val Phe Pro Asn Glu Val Gly Ala Arg Ile
165 170 175

Leu Thr Ser Glu Ser Gln Leu Thr Ile Thr Lys Glu Lys Lys Glu Glu
180 185 190

Leu Gln Asp Cys Lys Ile Ser Pro Leu Met Val Ala Tyr Met Leu Glu
195 200 205

Arg Glu Leu Val Arg Lys Thr Arg Phe Leu Pro Val Ala Gly Gly Thr
210 215 220

Ser Ser Val Tyr Ile Glu Val Leu His Leu Thr Gln Gly Thr Cys Trp
225 230 235 240

Glu Gln Met Tyr Thr Pro Gly Gly Glu Val Arg Asn Asp Asp Val Asp
245 250 255

Gln Ser Leu Ile Ile Ala Ala Arg Ser Ile Val Arg Arg Ala Ala Val
260 265 270

Ser Ala Asp Pro Leu Ala Ser Leu Leu Glu Met Cys His Ser Thr Gln
275 280 285

Ile Gly Gly Thr Arg Met Val Asp Ile Leu Arg Gln Asn Pro Thr Glu
290 295 300

Glu Gln Ala Val Glu Ile Cys Lys Ala Ala Met Gly Leu Arg Ile Ser
305 310 315 320

Ser Ser Phe Ser Phe Gly Gly Phe Thr Phe Lys Arg Thr Ser Gly Ser
325 330 335

Ser Val Lys Arg Glu Glu Glu Val Leu Thr Gly Asn Leu Gln Thr Leu
340 345 350

Lys Ile Arg Val His Glu Gly Tyr Glu Glu Phe Thr Met Val Gly Lys
355 360 365

Arg Ala Thr Ala Ile Leu Arg Lys Ala Thr Arg Arg Leu Ile Gln Leu
370 375 380

Ile Val Ser Gly Arg Asp Glu Gln Ser Ile Ala Glu Ala Ile Ile Val
385 390 395 400

Ala Met Val Phe Ser Gln Glu Asp Cys Met Ile Lys Ala Val Arg Gly
405 410 415

Asp Leu Asn Phe Val Asn Arg Ala Asn Gln Arg Leu Asn Pro Met His
420 425 430

Gln Leu Leu Arg His Phe Gln Lys Asp Ala Lys Val Leu Phe Gln Asn
435 440 445

Trp Gly Ile Glu His Ile Asp Asn Val Met Gly Met Ile Gly Val Leu
450 455 460

a)

Pro Asp Met Thr Pro Ser Thr Glu Met Ser Met Arg Gly Val Arg Val
465 470 475 480

Ser Lys Met Gly Val Asp Glu Tyr Ser Ser Ala Glu Arg Val Val Val
485 490 495

Ser Ile Asp Arg Phe Leu Arg Val Arg Asp Gln Arg Gly Asn Val Leu
500 505 510

Leu Ser Pro Glu Glu Val Ser Glu Thr Gln Gly Thr Glu Lys Leu Thr
515 520 525

Ile Thr Tyr Ser Ser Ser Met Met Trp Glu Ile Asn Gly Pro Glu Ser
530 535 540

Val Leu Val Asn Thr Tyr Gln Trp Ile Ile Arg Asn Trp Glu Thr Val
545 550 555 560

Lys Ile Gln Trp Ser Gln Asn Pro Thr Met Leu Tyr Asn Lys Met Glu
565 570 575

Phe Glu Pro Phe Gln Ser Leu Val Pro Lys Ala Ile Arg Gly Gln Tyr
580 585 590

Ser Gly Phe Val Arg Thr Leu Phe Gln Gln Met Arg Asp Val Leu Gly
595 600 605

Thr Phe Asp Thr Thr Gln Ile Ile Lys Leu Leu Pro Phe Ala Ala Ala
610 615 620

Pro Pro Lys Gln Ser Arg Met Gln Phe Ser Ser Leu Thr Val Asn Val
625 630 635 640

Arg Gly Ser Gly Met Arg Ile Leu Val Arg Gly Asn Ser Pro Ile Phe
645 650 655

Asn Tyr Asn Lys Thr Thr Lys Arg Leu Thr Ile Leu Gly Lys Asp Ala
660 665 670

Gly Thr Leu Thr Glu Asp Pro Asp Glu Gly Thr Ser Gly Val Glu Ser
675 680 685

Ala Val Leu Arg Gly Phe Leu Ile Leu Gly Lys Glu Asp Arg Arg Tyr
690 695 700

Gly Pro Ala Leu Ser Ile Asn Glu Leu Ser Asn Leu Ala Lys Gly Glu
705 710 715 720

Lys Ala Asn Val Leu Ile Gly Gln Gly Asp Val Val Leu Val Met Lys

725

730

735

Arg Lys Arg Asn Ser Ser Ile Leu Thr Asp Ser Gln Thr Ala Thr Lys
740 745 750

Arg Ile Arg Met Ala Ile Asn
755

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HA

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(144, "u")
- (D) OTHER INFORMATION: /gene= "HA"
/note= "u in ca "master" strain; a in
w2(3)"
/citation= ([1])

(ix) FEATURE:

- (A) NAME/KEY: mutation

(B) LOCATION: replace(455, "a")

(D) OTHER INFORMATION: /gene= "HA"
/note= "a in ca "master" strain; g in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(729, "c")
- (D) OTHER INFORMATION: /gene= "HA"
/note= "c in ca "master" strain; a in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 44..1729
- (D) OTHER INFORMATION: /product= "hemagglutinin"
/gene= "HA"
/note= "hemagglutinin protein"
/citation= ([1])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:17: FROM 1 TO 1773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCAAAAGCA GGGGUUAUAC CAUAGACAAC CAAAAGCAAA ACA AUG GCC AUC AUU
Met Ala Ile Ile

UAU CUC AUU CUC CUG UUC ACA GCA GUG AGA GGG GAC AAG AUA UGC AUU Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Asp Lys Ile Cys Ile 5 10 15 20	103
GGA UAC CAU GCC AAU AAU UCC ACA GAG ACG GUC GAC ACA AUU CUA GAG Gly Tyr His Ala Asn Asn Ser Thr Glu Thr Val Asp Thr Ile Leu Glu 25 30 35	151
CGG AAC GUC ACU GUG ACU CAU GCC AAG GAC AUU CUU GAG AAG ACC CAU Arg Asn Val Thr Val Thr His Ala Lys Asp Ile Leu Glu Lys Thr His 40 45 50	199
AAC GGA AAG UUA UGC AAA CUA AAC GGA AUC CCU CCA CUU GAA CUA GGG Asn Gly Lys Leu Cys Lys Leu Asn Gly Ile Pro Pro Leu Glu Leu Gly 55 60 65	247
GAC UGU AGC AUU GCC GGA UGG CUC CUU GGA AAU CCA GAA UGU GAU AGG Asp Cys Ser Ile Ala Gly Trp Leu Leu Gly Asn Pro Glu Cys Asp Arg 70 75 80	295
CUU CUA AGU GUG CCA GAA UGG UCC UAU AUA AUG GAG AAA GAA AAC CCG Leu Leu Ser Val Pro Glu Trp Ser Tyr Ile Met Glu Lys Glu Asn Pro 85 90 95 100	343
AGA AAC GGU UUG UGU UAU CCA GGC AAC UUC AAU GAU UAU GAA GAA UUG Arg Asn Gly Leu Cys Tyr Pro Gly Asn Phe Asn Asp Tyr Glu Glu Leu 105 110 115	391
AAA CAU CUC CUC AGC AGC GUG AAA CAU UUC GAG AAA GUA AAG AUU CUG Lys His Leu Leu Ser Ser Val Lys His Phe Glu Lys Val Lys Ile Leu 120 125 130	439
CCC AAA GAU AGA UGG ACA CAG CAU ACA ACA ACU GGA GGU UCA CAG GCC Pro Lys Asp Arg Trp Thr Gln His Thr Thr Gly Gly Ser Gln Ala 135 140 145	487
UGC GCG GUG UCU GGU AAU CCA UCA UUC UUC AGG AAC AUG GUC UGG CUG Cys Ala Val Ser Gly Asn Pro Ser Phe Phe Arg Asn Met Val Trp Leu 150 155 160	535
ACA GAG GAA GGA UCA AAU UAU CCG GUU GCC AAA GGA UCG UAC AAC AUU Thr Glu Glu Gly Ser Asn Tyr Pro Val Ala Lys Gly Ser Tyr Asn Asn 165 170 175 180	583
ACA AGC GGA GAA CAA AUG CUA AUA AUU UGG GGG GUG CAC CAU CCC AUU Thr Ser Gly Glu Gln Met Leu Ile Ile Trp Gly Val His His Pro Ile 185 190 195	631
GAU GAG ACA GAA CAA AGA ACA UUG UAC CAG AAU GUG GGA ACC UAU GUU Asp Glu Thr Glu Gln Arg Thr Leu Tyr Gln Asn Val Gly Thr Tyr Val 200 205 210	679
UCC GUA GGC ACA UCA ACA UUG AAC AAA AGG UCA ACC CCA GAA AUA GCA	727

Ser Val Gly Thr Ser Thr Leu Asn Lys Arg Ser Thr Pro Glu Ile Ala
215 220 225

ACA AGG CCU AAA GUG AAU GGA CUA GGA AGU AGA AUG GAA UUC UCU UGG
Thr Arg Pro Lys Val Asn Gly Leu Gly Ser Arg Met Glu Phe Ser Trp
230 235 240

775

ACC CUC UUG GAU AUG UGG GAC ACC AUA AAU UUU GAG AGU ACU GGU AAU
Thr Leu Leu Asp Met Trp Asp Thr Ile Asn Phe Glu Ser Thr Gly Asn
245 250 255 260

823

CUA AUU GCA CCA GAG UAU GGA UUC AAA AUA UCG AAA AGA GGU AGU UCU
Leu Ile Ala Pro Glu Tyr Gly Phe Lys Ile Ser Lys Arg Gly Ser Ser
265 270 275

871

GGG AUC AUG AAA ACA GAA GGA ACA CUU GAG AAC UGU GAG ACC AAA UGC
Gly Ile Met Lys Thr Glu Gly Thr Leu Glu Asn Cys Glu Thr Lys Cys
280 285 290

919

CAA ACU CCU UUG GGA GCA AUA AAU ACA ACA UUG CCU UUU CAC AAU GUC
Gln Thr Pro Leu Gly Ala Ile Asn Thr Thr Leu Pro Phe His Asn Val
295 300 305

967

CAC CCA CUG ACA AUA GGU GAG UGC CCC AAA UAU GUA AAA UCG GAG AAG
His Pro Leu Thr Ile Gly Glu Cys Pro Lys Tyr Val Lys Ser Glu Lys
310 315 320

1015

UUG GUC UUA GCA ACA GGA CUA AGG AAU GUU CCC CAG AUU GAA UCA AGA
Leu Val Leu Ala Thr Gly Leu Arg Asn Val Pro Gln Ile Glu Ser Arg
325 330 335 340

1063

GGA UUG UUU GGG GCA AUA GCU GGU UUU AUA GAA GGA GGA UGG CAA GGA
Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly
345 350 355

1111

AUG GUU GAU GGU UGG UAU GGA UAC CAU CAC AGC AAU GAC CAG GGA UCA
Met Val Asp Gly Trp Tyr Gly Tyr His His Ser Asn Asp Gln Gly Ser
360 365 370

1159

GGG UAU GCA GCA GAC AAA GAA UCC ACU CAA AAG GCA UUU GAU GGA AUC
Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala Phe Asp Gly Ile
375 380 385

1207

ACC AAC AAG GUA AAU UCU GUG AUU GAA AAG AUA AAC ACC CAA UUU GAA
Thr Asn Lys Val Asn Ser Val Ile Glu Lys Ile Asn Thr Gln Phe Glu
390 395 400

1255

GCU GUU GGG AAA GAA UUC AGU AAC UUA GAG AGA AGA CUG GAG AAC UUG
Ala Val Gly Lys Glu Phe Ser Asn Leu Glu Arg Arg Leu Glu Asn Leu
405 410 415 420

1303

AAC AAA AAG AUG GAA GAC GGG UUU CUA GAU GUG UGG ACA UAC AAU GCU
Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala
425 430 435

1351

GAG CUU CUA GUU CUG AUG GAA AAU GAG AGG ACA CUU GAC UUU CAU GAU 1399
Gl_u Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu Asp Phe His Asp
440 445 450

UCU AAU GUC AAG AAU CUG UAU GAU AAA GUC AGA AUG CAG CUG AGG GAC 1447
Ser Asn Val Lys Asn Leu Tyr Asp Lys Val Arg Met Gln Leu Arg Asp
455 460 465

AAC GUC AAA GAA CUA GGA AAU GGA UGU UUU GAA UUU UAU CAC AAA UGU 1495
Asn Val Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe Tyr His Lys Cys
470 475 480

GAU GAU GAA UGC AUG AAU AGU GUG AAA AAC GGG ACA UAU GAU UAU CCC 1543
Asp Asp Glu Cys Met Asn Ser Val Lys Asn Gly Thr Tyr Asp Tyr Pro
485 490 495 500

AAG UAU GAA GAA GAG UCU AAA CUA AAU AGA AAU GAA AUU AAA GGG GUA 1591
Lys Tyr Glu Glu Ser Lys Leu Asn Arg Asn Glu Ile Lys Gly Val
505 510 515

AAA UUG AGC AGC AUG GGG GUU UGU CGG AUC CUU GCC AUU UAU GCU ACA 1639
Lys Leu Ser Ser Met Gly Val Cys Arg Ile Leu Ala Ile Tyr Ala Thr
520 525 530

GUA GCA GGU UCU CUG UCA CUG GCA AUC AUG AUG GCU GGG AUC UCU UUC 1687
Val Ala Gly Ser Leu Ser Leu Ala Ile Met Met Ala Gly Ile Ser Phe
535 540 545

UGG AUG UGC UCC AAC GGG UCU CUG CAG UGC AGG AUC UGC AUA 1729
Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile Cys Ile
550 555 560

UGAUUUAAG UCAUUUAUA AUUAAAACA CCCUUGUUUC UACU 1773

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Asp
1 5 10 15

Lys Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Thr Val Asp
20 25 30

Thr Ile Leu Glu Arg Asn Val Thr Val Thr His Ala Lys Asp Ile Leu
35 40 45

Glu Lys Thr His Asn Gly Lys Leu Cys Lys Leu Asn Gly Ile Pro Pro
50 55 60

Leu Glu Leu Gly Asp Cys Ser Ile Ala Gly Trp Leu Leu Gly Asn Pro
65 70 75 80

Glu Cys Asp Arg Leu Leu Ser Val Pro Glu Trp Ser Tyr Ile Met Glu
85 90 95

Lys Glu Asn Pro Arg Asn Gly Leu Cys Tyr Pro Gly Asn Phe Asn Asp
100 105 110

Tyr Glu Glu Leu Lys His Leu Leu Ser Ser Val Lys His Phe Glu Lys
115 120 125

Val Lys Ile Leu Pro Lys Asp Arg Trp Thr Gln His Thr Thr Thr Gly
130 135 140

Gly Ser Gln Ala Cys Ala Val Ser Gly Asn Pro Ser Phe Phe Arg Asn
145 150 155 160

Met Val Trp Leu Thr Glu Glu Gly Ser Asn Tyr Pro Val Ala Lys Gly
165 170 175

Ser Tyr Asn Asn Thr Ser Gly Glu Gln Met Leu Ile Ile Trp Gly Val
180 185 190

His His Pro Ile Asp Glu Thr Glu Gln Arg Thr Leu Tyr Gln Asn Val
195 200 205

Gly Thr Tyr Val Ser Val Gly Thr Ser Thr Leu Asn Lys Arg Ser Thr
210 215 220

Pro Glu Ile Ala Thr Arg Pro Lys Val Asn Gly Leu Gly Ser Arg Met
225 230 235 240

Glu Phe Ser Trp Thr Leu Leu Asp Met Trp Asp Thr Ile Asn Phe Glu
245 250 255

Ser Thr Gly Asn Leu Ile Ala Pro Glu Tyr Gly Phe Lys Ile Ser Lys
260 265 270

Arg Gly Ser Ser Gly Ile Met Lys Thr Glu Gly Thr Leu Glu Asn Cys
275 280 285

Glu Thr Lys Cys Gln Thr Pro Leu Gly Ala Ile Asn Thr Thr Leu Pro
290 295 300

Phe His Asn Val His Pro Leu Thr Ile Gly Glu Cys Pro Lys Tyr Val

305 310 315 320
Lys Ser Glu Lys Leu Val Leu Ala Thr Gly Leu Arg Asn Val Pro Gln
 325 330 335
a
Ile Glu Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly
 340 345 350
Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His Ser Asn
 355 360 365
Asp Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala
 370 375 380
Phe Asp Gly Ile Thr Asn Lys Val Asn Ser Val Ile Glu Lys Ile Asn
 385 390 395 400
Thr Gln Phe Glu Ala Val Gly Lys Glu Phe Ser Asn Leu Glu Arg Arg
 405 410 415
Leu Glu Asn Leu Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp
 420 425 430
Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu
 435 440 445
Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr Asp Lys Val Arg Met
 450 455 460
Gln Leu Arg Asp Asn Val Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe
 465 470 475 480
Tyr His Lys Cys Asp Asp Glu Cys Met Asn Ser Val Lys Asn Gly Thr
 485 490 495
Tyr Asp Tyr Pro Lys Tyr Glu Glu Ser Lys Leu Asn Arg Asn Glu
 500 505 510
Ile Lys Gly Val Lys Leu Ser Ser Met Gly Val Cys Arg Ile Leu Ala
 515 520 525
Ile Tyr Ala Thr Val Ala Gly Ser Leu Ser Leu Ala Ile Met Met Ala
 530 535 540
Gly Ile Ser Phe Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile
 545 550 555 560
Cys Ile

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1467 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: NA

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(394, "u")
- (D) OTHER INFORMATION: /product= "Neuraminidase"
/gene= "NA"
/note= "u in ca "master" strain; c in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(604, "u")
- (D) OTHER INFORMATION: /product= "Neuraminidase"
/gene= "NA"
/note= "u in ca "master" strain; a in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 20..1426
- (D) OTHER INFORMATION: /product= "neuraminidase"
/gene= "NA"

/note= "neuraminidase protein"
/citation= ([1])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
- (B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) Influenza Virus
- (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
- (G) DATE: 1993
- (K) RELEVANT RESIDUES IN SEQ ID NO:19: FROM 1 TO 1467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCAAAAGCA GGAGUGAAA AUG AAU CCA AAU CAA AAG ACA AUA ACA AUU GGC	52
Met Asn Pro Asn Gln Lys Thr Ile Thr Ile Gly	
1 5 10	
UCU GUC UCU CUC ACC AUC GCA ACA GUA UGC UUC CUC AUG CAG AUU GCC	100
Ser Val Ser Leu Thr Ile Ala Thr Val Cys Phe Leu Met Gln Ile Ala	
15 20 25	
AUC CUG GCA ACU ACU GUG ACA UUG CAC CUU AAG CAA CAU GAG UGC GAC	148
Ile Leu Ala Thr Thr Val Thr Leu His Leu Lys Gln His Glu Cys Asp	
30 35 40	
UCC CCC GCG AGC AAC CAA GUA AUG CCA UGU GAA CCA AUA AUA AUA GAA	196
Ser Pro Ala Ser Asn Gln Val Met Pro Cys Glu Pro Ile Ile Ile Glu	
45 50 55	
AGG AAC AUA ACA GAG AUA GUG UAU UUG AAU AAC ACC ACC AUA GAG AAA	244
Arg Asn Ile Thr Glu Ile Val Tyr Leu Asn Asn Thr Thr Ile Glu Lys	
60 65 70 75	
GAG AUU UGC CCC GAA GUA GUG GGA UAC AGA AAU UGG UCA AAG CCG CAA	292
Glu Ile Cys Pro Glu Val Val Gly Tyr Arg Asn Trp Ser Lys Pro Gln	
80 85 90	
UGU CAA AUU ACA GGA UUU GCA CCU UUU UCU AAG GAC AAU UCA AUC CGG	340
Cys Gln Ile Thr Gly Phe Ala Pro Phe Ser Lys Asp Asn Ser Ile Arg	
95 100 105	
CUU UCU GCU GGU GGG GAC AUU UGG GUG ACG AGA GAA CCU UAU GUG UCA	388
Leu Ser Ala Gly Gly Asp Ile Trp Val Thr Arg Glu Pro Tyr Val Ser	
110 115 120	

UGC GAU CCU GGC AAG UGU UAU CAA UUU GCA CUC GGG CAG GGG ACC ACA Cys Asp Pro Gly Lys Cys Tyr Gln Phe Ala Leu Gly Gln Gly Thr Thr 125 130 135	436
<i>Al</i> CUA GAC AAC AAA CAU UCA AAU GGC ACA AUA CAU GAU AGA AUC CCU CAU Leu Asp Asn Lys His Ser Asn Gly Thr Ile His Asp Arg Ile Pro His 140 145 150 155	484
CGA ACC CUA UUA AUG AAU GAG UUG GGU GUU CCA UUU CAU UUA GGA ACC Arg Thr Leu Leu Met Asn Glu Leu Gly Val Pro Phe His Leu Gly Thr 160 165 170	532
AAA CAA GUG UGU GCA GCA UGG UCC AGC UCA AGU UGU CAC GAU GGA AAA Lys Gln Val Cys Ala Ala Trp Ser Ser Ser Cys His Asp Gly Lys 175 180 185	580
GCA UGG UUG CAU GUU UGU GUC ACU GGG GAU GAU AGA AAU GCA ACU GCU Ala Trp Leu His Val Cys Val Thr Gly Asp Asp Arg Asn Ala Thr Ala 190 195 200	628
AGC UUC AUU UAU GAC GGG AAG CUU GUG GAC AGU AAU GGU UCA UGG UCU Ser Phe Ile Tyr Asp Gly Lys Leu Val Asp Ser Ile Gly Ser Trp Ser 205 210 215	676
CAA AAU GUC CUC AGG ACC CAG GAG UCG GAA UGC GUC UGU AUC AAU GGG Gln Asn Val Leu Arg Thr Gln Glu Ser Glu Cys Val Cys Ile Asn Gly 220 225 230 235	724
ACU UGC ACA GUA GUA AUG ACU GAU GGA AGU GCA UCA GGA AGA GCU GAU Thr Cys Thr Val Val Met Thr Asp Gly Ser Ala Ser Gly Arg Ala Asp 240 245 250	772
ACU AGA AUA CUA UUC AUU AAA GAG GGG AAA AAU GUC CAU AAU GGC CCA Thr Arg Ile Leu Phe Ile Lys Glu Gly Lys Ile Val His Ile Gly Pro 255 260 265	820
UUG UCA GGA AGU GCU CAG CAU GUA GAG GAG UGU UCU UGU UAC CCU CGA Leu Ser Gly Ser Ala Gln His Val Glu Glu Cys Ser Cys Tyr Pro Arg 270 275 280	868
UAU CCU GAC GUC AGA UGU AUC UGC AGA GAC AAC UGG AAA GGC UCU AAU Tyr Pro Asp Val Arg Cys Ile Cys Arg Asp Asn Trp Lys Gly Ser Asn 285 290 295	916
AGG CCC GUU AUA GAC AUA AAU AUG GAA GAU UAU AGC AAU GAU UCC AGU Arg Pro Val Ile Asp Ile Asn Met Glu Asp Tyr Ser Ile Asp Ser Ser 300 305 310 315	964
UAU GUG UGC UCA GGG CUU GUU GGC GAC ACA CCC AGG AAC GAC GAC AGC Tyr Val Cys Ser Gly Leu Val Gly Asp Thr Pro Arg Asn Asp Asp Ser 320 325 330	1012
UCU AGC AAU AGC AAU UGC AGG GAU CCU AAC AAU GAG AGA GGG AAU CCA Ser Ser Asn Ser Asn Cys Arg Asp Pro Asn Asn Glu Arg Gly Asn Pro 335 340 345	1060

Gly Val Lys Gly Trp Ala Phe Asp Asn Gly Asp Asp Val Trp Met Gly 1108
350 355 360

Arg Thr Ile Ser Lys Asp Leu Arg Ser Gly Tyr Glu Thr Phe Lys Val 1156
365 370 375

Ile Gly Gly Trp Ser Thr Pro Asn Ser Lys Ser Gln Val Asn Arg Gln 1204
380 385 390 395

Val Ile Val Asp Asn Asn Trp Ser Gly Tyr Ser Gly Ile Phe Ser 1252
400 405 410

Val Glu Gly Lys Ser Cys Ile Asn Arg Cys Phe Tyr Val Glu Leu Ile 1300
415 420 425

Arg Gly Arg Pro Gln Glu Thr Arg Val Trp Trp Thr Ser Asn Ser Ile 1348
430 435 440

Val Val Phe Cys Gly Thr Ser Gly Thr Tyr Gly Thr Gly Ser Trp Pro 1396
445 450 455

Asp Gly Ala Asn Ile Asn Phe Met Pro Ile 1446
460 465

AAAAAACUCC UUGUUUCUAC U 1467

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Asn Pro Asn Gln Lys Thr Ile Thr Ile Gly Ser Val Ser Leu Thr
1 5 10 15

Ile Ala Thr Val Cys Phe Leu Met Gln Ile Ala Ile Leu Ala Thr Thr
20 25 30

Val Thr Leu His Leu Lys Gln His Glu Cys Asp Ser Pro Ala Ser Asn
35 40 45

Gln Val Met Pro Cys Glu Pro Ile Ile Glu Arg Asn Ile Thr Glu
50 55 60

Ile Val Tyr Leu Asn Asn Thr Thr Ile Glu Lys Glu Ile Cys Pro Glu
65 70 75 80

Val Val Gly Tyr Arg Asn Trp Ser Lys Pro Gln Cys Gln Ile Thr Gly
85 90 95

Phe Ala Pro Phe Ser Lys Asp Asn Ser Ile Arg Leu Ser Ala Gly Gly
100 105 110

Asp Ile Trp Val Thr Arg Glu Pro Tyr Val Ser Cys Asp Pro Gly Lys
115 120 125

Cys Tyr Gln Phe Ala Leu Gly Gln Gly Thr Thr Leu Asp Asn Lys His
130 135 140

Ser Asn Gly Thr Ile His Asp Arg Ile Pro His Arg Thr Leu Leu Met
145 150 155 160

Asn Glu Leu Gly Val Pro Phe His Leu Gly Thr Lys Gln Val Cys Ala
165 170 175

Ala Trp Ser Ser Ser Cys His Asp Gly Lys Ala Trp Leu His Val
180 185 190

Cys Val Thr Gly Asp Asp Arg Asn Ala Thr Ala Ser Phe Ile Tyr Asp
195 200 205

Gly Lys Leu Val Asp Ser Ile Gly Ser Trp Ser Gln Asn Val Leu Arg
210 215 220

Thr Gln Glu Ser Glu Cys Val Cys Ile Asn Gly Thr Cys Thr Val Val
225 230 235 240

Met Thr Asp Gly Ser Ala Ser Gly Arg Ala Asp Thr Arg Ile Leu Phe
245 250 255

Ile Lys Glu Gly Lys Ile Val His Ile Gly Pro Leu Ser Gly Ser Ala
260 265 270

Gln His Val Glu Glu Cys Ser Cys Tyr Pro Arg Tyr Pro Asp Val Arg
275 280 285

Cys Ile Cys Arg Asp Asn Trp Lys Gly Ser Asn Arg Pro Val Ile Asp
290 295 300

Ile Asn Met Glu Asp Tyr Ser Ile Asp Ser Ser Tyr Val Cys Ser Gly

305 310 315 320
Leu Val Gly Asp Thr Pro Arg Asn Asp Asp Ser Ser Ser Asn Ser Asn
 325 330 335
Cys Arg Asp Pro Asn Asn Glu Arg Gly Asn Pro Gly Val Lys Gly Trp
 340 345 350
Ala Phe Asp Asn Gly Asp Asp Val Trp Met Gly Arg Thr Ile Ser Lys
 355 360 365
Asp Leu Arg Ser Gly Tyr Glu Thr Phe Lys Val Ile Gly Gly Trp Ser
 370 375 380
Thr Pro Asn Ser Lys Ser Gln Val Asn Arg Gln Val Ile Val Asp Asn
 385 390 395 400
Asn Asn Trp Ser Gly Tyr Ser Gly Ile Phe Ser Val Glu Gly Lys Ser
 405 410 415
Cys Ile Asn Arg Cys Phe Tyr Val Glu Leu Ile Arg Gly Arg Pro Gln
 420 425 430
Glu Thr Arg Val Trp Trp Thr Ser Asn Ser Ile Val Val Phe Cys Gly
 435 440 445
Thr Ser Gly Thr Tyr Gly Thr Gly Ser Trp Pro Asp Gly Ala Asn Ile
 450 455 460
Asn Phe Met Pro Ile
 465

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 890 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: NS

6
(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 27..56

(D) OTHER INFORMATION: /product= "nonstructural protein NS2"
/gene= "NS"
/note= "nonstructural protein NS2"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(483, "a")

(D) OTHER INFORMATION: /note= "a in ca "master" strain and in
wt2(3); g in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 529..861

(D) OTHER INFORMATION: /product= "nonstructural protein NS2"
/gene= "NS"
/note= "nonstructural protein NS2"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(813, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); a in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

- (B) LOCATION: join(27..56, 529..861)
- (D) OTHER INFORMATION: /product= "nonstructural protein NS2"
/gene= "NS"
/note= "nonstructural protein NS2"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 27..677
- (D) OTHER INFORMATION: /product= "nonstructural protein NS1"
/gene= "NS"
/note= "nonstructural protein NS1"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
- (B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) influenza virus
- (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
- (G) DATE: 1993,
- (K) RELEVANT RESIDUES IN SEQ ID NO:21: FROM 1 TO 890

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C
- (B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza vaccine strain, A/Ann Arbor/6/60(H2N2)
- (C) JOURNAL: Virology
- (D) VOLUME: 167
- (F) PAGES: 554-567
- (G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:21: FROM 1 TO 890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGCAAAAGCA GGGUGACAAA GACAUA AUG GAU CCU AAC ACU GUG UCA AGC UUU Met Asp Pro Asn Thr Val Ser Ser Phe	53
1 5	
CAG GUA GAU UGC UUC CUU UGG CAU GUC CGC AAA CAA GUU GCA GAC CAA Gln Val Asp Cys Phe Leu Trp His Val Arg Lys Gln Val Ala Asp Gln	101
10 15 20 25	
GAA CUA GGU GAU GCC CCA UUC CUU GAU CGG CUU CGC CGA GAU CAG AAG Glu Leu Gly Asp Ala Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys	149
30 35 40	
UCC CUA AGG GGA AGA GGC AGU ACU CUC GGU CUG AAC AUC GAA ACA GCC Ser Leu Arg Gly Arg Ser Thr Leu Gly Leu Asn Ile Glu Thr Ala	197
45 50 55	
ACC CGU GUU GGA AAG CAG AUA GUG GAG AGG AUU CUG AAG GAA GAA UCC Thr Arg Val Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser	245
60 65 70	
GAU GAG GCA CUU AAA AUG ACC AUG GCC UCC GCA CCU GCU UCG CGA UAC Asp Glu Ala Leu Lys Met Thr Met Ala Ser Ala Pro Ala Ser Arg Tyr	293
75 80 85	
CUA ACU GAC AUG ACU AUU GAG GAA AUG UCA AGG GAC UGG UUC AUG CUA Leu Thr Asp Met Thr Ile Glu Glu Met Ser Arg Asp Trp Phe Met Leu	341
90 95 100 105	
AUG CCC AAG CAG AAA GUG GCA GGC CCU CUU UGU AUC AGA AUG GAC CAG Met Pro Lys Gln Lys Val Ala Gly Pro Leu Cys Ile Arg Met Asp Gln	389
110 115 120	
GCA AUC AUG GAU AAG AAC AUC AUA UUG AAA GCG AAU UUC AGU GUG AUU Ala Ile Met Asp Lys Asn Ile Ile Leu Lys Ala Asn Phe Ser Val Ile	437
125 130 135	
UUU GAC CGG CUA GAG ACC CUA AUA UUA CUA AGG GCU UUC ACC GAA ACG Phe Asp Arg Leu Glu Thr Leu Ile Leu Leu Arg Ala Phe Thr Glu Thr	485
140 145 150	
GGA GCA AUU GUU GGC GAA AUU UCA CCA UUG CCU UCU CUU CCA GGA CAU Gly Ala Ile Val Gly Glu Ile Ser Pro Leu Pro Ser Leu Pro Gly His	533
155 160 165	
ACU AAU GAG GAU GUC AAA AAU GCA AAU GGG GUC CUC AUC GGA GGA CUU Thr Asn Glu Asp Val Lys Asn Ala Ile Gly Val Leu Ile Gly Gly Leu	581
170 175 180 185	
GAA UGG AAU GAU AAC ACA GUU CGA GUC UCU AAA ACU CUA CAG AGA UUC Glu Trp Asn Asp Asn Thr Val Arg Val Ser Lys Thr Leu Gln Arg Phe	629

190

195

200

GCU UGG AGA AGC AGU GAU GAG AAU GGG AGA CCU CCA CUC ACU CCA AAA
Ala Trp Arg Ser Ser Asp Glu Asn Gly Arg Pro Pro Leu Thr Pro Lys
205 210 215

677

UAGAAACGGA AAAUGGCGAG AACAAUUAGG UCAAAAGUUC GAAGAAUUA GAUGGCUGAU
UGAAGAACUG AGACACAAAU UGAAGAUAC AGAGAAUAGU UUUGAGCAA UAACAUUUAU
GCAAGCCUUA CAGCUGCUAU UUGAAGUGGA ACAAGAGAUA AGAACUUUCU CGUUUCAGCU
UAUUUAAUGA UAAAAAACAC CCUUGUUUCU ACU

737

797

857

890

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys Phe Leu Trp
1 5 10 15

His Val Arg Lys Gln Val Ala Asp Gln Glu Leu Gly Asp Ala Pro Phe
20 25 30

Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly Arg Gly Ser
35 40 45

Thr Leu Gly Leu Asn Ile Glu Thr Ala Thr Arg Val Gly Lys Gln Ile
50 55 60

Val Glu Arg Ile Leu Lys Glu Glu Ser Asp Glu Ala Leu Lys Met Thr
65 70 75 80

Met Ala Ser Ala Pro Ala Ser Arg Tyr Leu Thr Asp Met Thr Ile Glu
85 90 95

Glu Met Ser Arg Asp Trp Phe Met Leu Met Pro Lys Gln Lys Val Ala
100 105 110

Gly Pro Leu Cys Ile Arg Met Asp Gln Ala Ile Met Asp Lys Asn Ile
115 120 125

Ile Leu Lys Ala Asn Phe Ser Val Ile Phe Asp Arg Leu Glu Thr Leu
130 135 140

Ile Leu Leu Arg Ala Phe Thr Glu Thr Gly Ala Ile Val Gly Glu Ile
145 150 155 160

Ser Pro Leu Pro Ser Leu Pro Gly His Thr Asn Glu Asp Val Lys Asn
165 170 175

Ala Ile Gly Val Leu Ile Gly Gly Leu Glu Trp Asn Asp Asn Thr Val
180 185 190

Arg Val Ser Lys Thr Leu Gln Arg Phe Ala Trp Arg Ser Ser Asp Glu
195 200 205

Asn Gly Arg Pro Pro Leu Thr Pro Lys
210 215

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 27..389
- (D) OTHER INFORMATION: /product= "Nonstructural protein 2"
/gene= "NS2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGCAAAAGCA GGGUGACAAA GACAUA AUG GAU CCU AAC ACU GUG UCA AGC UUU 53
Met Asp Pro Asn Thr Val Ser Ser Phe
1 5

CAG GAC AUA CUA AUG AGG AUG UCA AAA AUG CAA UUG GGG UCC UCA UCG 101
Gln Asp Ile Leu Met Arg Met Ser Lys Met Gln Leu Gly Ser Ser Ser
10 15 20 25

GAG GAC UUG AAU GGA AUG AUA ACA CAG UUC GAG UCU CUA AAA CUC UAC 149

Glu Asp Leu Asn Gly Met Ile Thr Gln Phe Glu Ser Leu Lys Leu Tyr	30	35	40	
AGA GAU UCG CUU GGA GAA GCA GUG AUG AGA AUG GGA GAC CUC CAC UCA				197
Arg Asp Ser Leu Gly Glu Ala Val Met Arg Met Gly Asp Leu His Ser	45	50	55	
CUC CAA AAU AGA AAC GGA AAA UGG CGA GAA CAA UUA GGU CAA AAG UUC				245
Leu Gln Asn Arg Asn Gly Lys Trp Arg Glu Gln Leu Gly Gln Lys Phe	60	65	70	
GAA GAA AUA AGA UGG CUG AUU GAA GAA GUG AGA CAC AAA UUG AAG AUA				293
Glu Glu Ile Arg Trp Leu Ile Glu Glu Val Arg His Lys Leu Lys Ile	75	80	85	
ACA GAG AAU AGU UUU GAG CAA AUA ACA UUU AUG CAA GCC UUA CAG CUG				341
Thr Glu Asn Ser Phe Glu Gln Ile Thr Phe Met Gln Ala Leu Gln Leu	90	95	100	
90	95	100	105	
CUA UUU GAA GUG GAA CAA GAG AUA AGA ACU UUC UCG UUU CAG CUU AUU				389
Leu Phe Glu Val Glu Gln Glu Ile Arg Thr Phe Ser Phe Gln Leu Ile	110	115	120	
UAAUGAUAAA AAACACCCUU GUUUCUACU				418

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Asp Pro Asn Thr Val Ser Ser Phe Gln Asp Ile Leu Met Arg Met	1	5	10	15
Ser Lys Met Gln Leu Gly Ser Ser Glu Asp Leu Asn Gly Met Ile	20	25	30	
Thr Gln Phe Glu Ser Leu Lys Leu Tyr Arg Asp Ser Leu Gly Glu Ala	35	40	45	
Val Met Arg Met Gly Asp Leu His Ser Leu Gln Asn Arg Asn Gly Lys	50	55	60	
Trp Arg Glu Gln Leu Gly Gln Lys Phe Glu Glu Ile Arg Trp Leu Ile				

65 70 75 80
Glu Glu Val Arg His Lys Leu Lys Ile Thr Glu Asn Ser Phe Glu Gln
 85 90 95
Ile Thr Phe Met Gln Ala Leu Gln Leu Leu Phe Glu Val Glu Gln Glu
 100 105 110
Ile Arg Thr Phe Ser Phe Gln Leu Ile
 115 120

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: M

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 26..51
- (D) OTHER INFORMATION: /product= "matrix protein M2"
 /gene= "M"
 /note= "matrix protein M2"
 /citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: exon

- (B) LOCATION: 740..1004
- (D) OTHER INFORMATION: /product= "matrix protein M2"
/gene= "M"
/note= "matrix protein M2"
/citation= ([1][2])

a1
(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(969, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3); g in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(26..51, 740..1004)
- (D) OTHER INFORMATION: /product= "matrix protein M2"
/gene= "M"
/note= "matrix protein M2"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 26..781
- (D) OTHER INFORMATION: /product= "matrix protein M1"
/gene= "M"
/note= "matrix protein M1"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
- (B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) influenza virus
- (C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:25: FROM 1 TO 1027

a
(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza vaccine strain, A/Ann Arbor/6/60(H2N2)

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-557

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:25: FROM 1 TO 1027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGCAAAAGCA GGUAGAUUU GAAAG AUG AGU CUU CUA ACC GAG GUC GAA ACG Met Ser Leu Leu Thr Glu Val Glu Thr	52
1 5	
UAC GUU CUC UCU AUC AUC CCG UCA GGC CCC CUC AAA GCC GAG AUC GCA Tyr Val Leu Ser Ile Ile Pro Ser Gly Pro Leu Lys Ala Glu Ile Ala	100
10 15 20 25	
CAG AGA CUU GAA GAU GUC UUU GCU GGG AAA AAC ACC GAU CUU GAG GCU Gln Arg Leu Glu Asp Val Phe Ala Gly Lys Asn Thr Asp Leu Glu Ala	148
30 35 40	
CUC AUG GAA UGG CUA AAG ACA AGA CCA AUC CUG UCA CCU CUG ACU AAG Leu Met Glu Trp Leu Lys Thr Arg Pro Ile Leu Ser Pro Leu Thr Lys	196
45 50 55	
GGG AUU UUG GGA UUU GUA UUC ACG CUC ACC GUG CCC AGU GAG CGA GGA Gly Ile Leu Gly Phe Val Phe Thr Leu Thr Val Pro Ser Glu Arg Gly	244
60 65 70	
CUG CAG CGU AGA CGC UUU GUC CAA AAU GCC CUC AAU GGG AAU GGG GAU Leu Gln Arg Arg Arg Phe Val Gln Asn Ala Leu Asn Gly Asn Gly Asp	292
75 80 85	
CCA AAU AAC AUG GAC AGA GCA GUU AAA CUG UAU AGA AAG CUU AAG AGG	340

Pro Asn Asn Met Asp Arg Ala Val Lys Leu Tyr Arg Lys Leu Lys Arg		
90 95 100 105		
GAG AUA ACA UUC CAU GGG GCC AAA GAA AUA GCG CUC AGU UAU UCU GCU	388	
Glu Ile Thr Phe His Gly Ala Lys Glu Ile Ala Leu Ser Tyr Ser Ala		
110 115 120		
GGU GCA CUU GCC AGU UGU AUG GGC CUC AUA UAC AAC AGG AUG GGG GCU	436	
Gly Ala Leu Ala Ser Cys Met Gly Leu Ile Tyr Asn Arg Met Gly Ala		
125 130 135		
GUG ACC ACU GAA GUG GUC UUA GGC CUG GUA UGU GCA ACC UGU GAA CAG	484	
Val Thr Thr Glu Val Val Leu Gly Leu Val Cys Ala Thr Cys Glu Gln		
140 145 150		
AUU GCU GAC UCC CAG CAU AGG UCU CAU AGG CAA AUG GUG ACA ACA ACC	532	
Ile Ala Asp Ser Gln His Arg Ser His Arg Gln Met Val Thr Thr Thr		
155 160 165		
AAU CCA CUA AUA AGA CAU GAG AAC AGA AUG GUU CUG GCC AGC ACU ACA	580	
Asn Pro Leu Ile Arg His Glu Asn Arg Met Val Leu Ala Ser Thr Thr		
170 175 180 185		
GCU AAG GCU AUG GAG CAA AUG GCU GGA UCG AGU GAG CAA GCA GCA GAG	628	
Ala Lys Ala Met Glu Gln Met Ala Gly Ser Ser Glu Gln Ala Ala Glu		
190 195 200		
GCC AUG GAG GUU GCU AGU CAG GCC AGG CAA AUG GUG CAG GCA AUG AGA	676	
Ala Met Glu Val Ala Ser Gln Ala Arg Gln Met Val Gln Ala Met Arg		
205 210 215		
GUU AUU GGG ACU CAU CCU AGC UCC AGU GCU GGU CUA AAA AAU GAU CUU	724	
Val Ile Gly Thr His Pro Ser Ser Ala Gly Leu Lys Asn Asp Leu		
220 225 230		
CUU GAA AAU UUG CAG GCC UAU CAG AAA CGA AUG GGG GUG CAG AUG CAA	772	
Leu Glu Asn Leu Gln Ala Tyr Gln Lys Arg Met Gly Val Gln Met Gln		
235 240 245		
CGA UUC AAG UGACCCUCUU GUUGUUGCCG CGAGUAUCAU UGGGAUCUUG	821	
Arg Phe Lys		
250		
CACUUGAUAU UGUGGAUUCU UGAUCAUCUU UUUUUCAAAU GCAUUUAUCG CUUCUUUAAA	881	
CACGGUCUGA AAAGAGGGCC UUCUACGGAA GGAGUACCAG AGUCUAUGAG GGAAGAAUAU	941	
CGAAAGGAAC AGCAGAGUGC UGUGGAUUCU GACGAUAGUC AUUUGUCAG CAUAGAGCUG	1001	
GAGUAAAAAA CUACCUUGUU UCUACU	1027	

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ser Leu Leu Thr Glu Val Glu Thr Tyr Val Val Leu Ser Ile Ile Pro
1 5 10 15

Ser Gly Pro Leu Lys Ala Glu Ile Ala Gln Arg Leu Glu Asp Val Phe
20 25 30

Ala Gly Lys Asn Thr Asp Leu Glu Ala Leu Met Glu Trp Leu Lys Thr
35 40 45

Arg Pro Ile Leu Ser Pro Leu Thr Lys Gly Ile Leu Gly Phe Val Phe
50 55 60

Thr Leu Thr Val Pro Ser Glu Arg Gly Leu Gln Arg Arg Arg Phe Val
65 70 75 80

Gln Asn Ala Leu Asn Gly Asn Gly Asp Pro Asn Asn Met Asp Arg Ala
85 90 95

Val Lys Leu Tyr Arg Lys Leu Lys Arg Glu Ile Thr Phe His Gly Ala
100 105 110

Lys Glu Ile Ala Leu Ser Tyr Ser Ala Gly Ala Leu Ala Ser Cys Met
115 120 125

Gly Leu Ile Tyr Asn Arg Met Gly Ala Val Thr Thr Glu Val Val Leu
130 135 140

Gly Leu Val Cys Ala Thr Cys Glu Gln Ile Ala Asp Ser Gln His Arg
145 150 155 160

Ser His Arg Gln Met Val Thr Thr Asn Pro Leu Ile Arg His Glu
165 170 175

Asn Arg Met Val Leu Ala Ser Thr Thr Ala Lys Ala Met Glu Gln Met
180 185 190

Ala Gly Ser Ser Glu Gln Ala Ala Glu Ala Met Glu Val Ala Ser Gln
195 200 205

Ala Arg Gln Met Val Gln Ala Met Arg Val Ile Gly Thr His Pro Ser
210 215 220

Ser Ser Ala Gly Leu Lys Asn Asp Leu Leu Glu Asn Leu Gln Ala Tyr
225 230 235 240

Gln Lys Arg Met Gly Val Gln Met Gln Arg Phe Lys
245 250

a)
(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 26..316
- (D) OTHER INFORMATION: /product= "Matrix M2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGCAAAAGCA GGUAGAUUU GAAAG AUG AGU CUU CUA ACC GAG GUC GAA ACG Met Ser Leu Leu Thr Glu Val Glu Thr	52
1 5	
CCU AUC AGA AAC GAA UGG GGG UGC AGA UGC AAC GAU UCA AGU GAC CCU Pro Ile Arg Asn Glu Trp Gly Cys Arg Cys Asn Asp Ser Ser Asp Pro	100
10 15 20 25	
CUU GUU GUU GCC GCG AGU AUC AUU GGG AUC UUG CAC UUG AUA UUG UGG Leu Val Val Ala Ala Ser Ile Ile Gly Ile Leu His Leu Ile Leu Trp	148
30 35 40	
AUU CUU GAU CAU CUU UUU UUC AAA UGC AUU UAU CGC UUC UUU AAA CAC Ile Leu Asp His Leu Phe Phe Lys Cys Ile Tyr Arg Phe Phe Lys His	196
45 50 55	
GGU CUG AAA AGA GGG CCU UCU ACG GAA GGA GUA CCA GAG UCU AUG AGG Gly Leu Lys Arg Gly Pro Ser Thr Glu Gly Val Pro Glu Ser Met Arg	244
60 65 70	

GAA GAA UAU CGA AAG GAA CAG CAG AGU GCU GUG GAU UCU GAC GAU AGU
Glu Glu Tyr Arg Lys Glu Gln Gln Ser Ala Val Asp Ser Asp Asp Ser 292
75 80 85

CAU UUU GUC AGC AUA GAG CUG GAG UAAAAAACUA CCUUGUUUCU ACU
His Phe Val Ser Ile Glu Leu Glu 339
90 95

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly
1 5 10 15

Cys Arg Cys Asn Asp Ser Ser Asp Pro Leu Val Val Ala Ala Ser Ile
20 25 30

Ile Gly Ile Leu His Leu Ile Leu Trp Ile Leu Asp His Leu Phe Phe
35 40 45

Lys Cys Ile Tyr Arg Phe Phe Lys His Gly Leu Lys Arg Gly Pro Ser
50 55 60

Thr Glu Gly Val Pro Glu Ser Met Arg Glu Glu Tyr Arg Lys Glu Gln
65 70 75 80

Gln Ser Ala Val Asp Ser Asp Asp Ser His Phe Val Ser Ile Glu Leu
85 90 95

Glu

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2341 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Influenza virus

(B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) egg passage 2(3)

(vii) IMMEDIATE SOURCE:

(B) CLONE: PB2

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(141, "a")

(D) OTHER INFORMATION: /note= "g in ca "master" strain; a in wt2(3); a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(426, "c")

(D) OTHER INFORMATION: /note= "c in ca "master" strain and in wt2(3); u in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(714, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3); c in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(821, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(963, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1182, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3); a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1212, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3); c in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1353, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in

wt2(3); u in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1923, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); a in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(1933, "u")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain; u in
wt2(3); u in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 28..2304
- (D) OTHER INFORMATION: /product= "polymerase basic 2"
/gene= "PB2"
/note= "polymerase basic 2"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
- (B) TITLE: Molecular and biological changes in the cold
adapted master strain A/AA/6/60 (H2N2) influenza virus
- (C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA
- (G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:29: FROM 1 TO 2341

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza vaccine strain, A/Ann Arbor/6/60(H2N2)

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:29: FROM 1 TO 2341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGCGAAAGCA GGUCAUUUAU AUUCAAU AUG GAA AGA AUA AAA GAA CUA CGG	51
Met Glu Arg Ile Lys Glu Leu Arg	
1 5	
AAU CUG AUG UCG CAG UCU CGC ACU CGC GAG AUA CUA ACA AAA ACC ACA	99
Asn Leu Met Ser Gln Ser Arg Thr Arg Glu Ile Leu Thr Lys Thr Thr	
10 15 20	
GUG GAC CAU AUG GCC AUA AUU AAG AAG UAC ACA UCA GGG AGA CAG GAA	147
Val Asp His Met Ala Ile Ile Lys Lys Tyr Thr Ser Gly Arg Gln Glu	
25 30 35 40	
AAG AAC CCG UCA CUU AGG AUG AAA UGG AUG AUG GCA AUG AAA UAU CCG	195
Lys Asn Pro Ser Leu Arg Met Lys Trp Met Met Ala Met Lys Tyr Pro	
45 50 55	
AUU ACA GCC GAC AAG AGG AUA ACA GAA AUG AUU CCU GAG AGA AAU GAG	243
Ile Thr Ala Asp Lys Arg Ile Thr Glu Met Ile Pro Glu Arg Asn Glu	
60 65 70	
CAA GGG CAA ACU CUA UGG AGU AAA AUG AGU GAU GCC GGA UCG GAU CGU	291
Gln Gly Gln Thr Leu Trp Ser Lys Met Ser Asp Ala Gly Ser Asp Arg	
75 80 85	
GUG AUG GUA UCA CCU CUG GCU GUG ACA UGG UGG AAU AGA AAU GGA CCA	339
Val Met Val Ser Pro Leu Ala Val Thr Trp Trp Asn Arg Asn Gly Pro	

90	95	100	
AUG ACA AGU ACG GUU CAU UAU CCA AAA AUC UAC AAA ACU UAU UUU GAG Met Thr Ser Thr Val His Tyr Pro Lys Ile Tyr Lys Thr Tyr Phe Glu 105 110 115 120			387
AAA GUC GAA AGG UUA AAA CAU GGA ACC UUU GGC CCU GUC CAU UUU AGA Lys Val Glu Arg Leu Lys His Gly Thr Phe Gly Pro Val His Phe Arg 125 130 135			435
AAC CAA GUC AAA AUA CGC CGA AGA GUU GAC AUA AAU CCU GGU CAU GCA Asn Gln Val Lys Ile Arg Arg Val Asp Ile Asn Pro Gly His Ala 140 145 150			483
GAC CUC AGU GCC AAG GAG GCA CAG GAU GUA AUC AUG GAA GUU GUU UUC Asp Leu Ser Ala Lys Glu Ala Gln Asp Val Ile Met Glu Val Val Phe 155 160 165			531
CCU AAC GAA GUG GGG GCC AGG AUA CUA ACG UCG GAA UCG CAA UUA ACA Pro Asn Glu Val Gly Ala Arg Ile Leu Thr Ser Glu Ser Gln Leu Thr 170 175 180			579
AUA ACC AAA GAG AAA AAA GAA CUC CAG GAU UGC AAA AUU UCA CCU Ile Thr Lys Glu Lys Glu Glu Leu Gln Asp Cys Lys Ile Ser Pro 185 190 195 200			627
UUG AUG GUU GCG UAC AUG UUA GAG AGA GAA CUU GUC CGA AAA ACG AGA Leu Met Val Ala Tyr Met Leu Glu Arg Glu Leu Val Arg Lys Thr Arg 205 210 215			675
UUU CUC CCA GUU GCU GGU GGA ACA AGC AGU GUG UAC AUU GAA GUG UUG Phe Leu Pro Val Ala Gly Gly Thr Ser Ser Val Tyr Ile Glu Val Leu 220 225 230			723
CAC UUG ACU CAA GGA ACA UGC UGG GAA CAG AUG UAC ACU CCA GGU GGA His Leu Thr Gln Gly Thr Cys Trp Glu Gln Met Tyr Thr Pro Gly Gly 235 240 245			771
GAA GUG AGG AAU GAU GAU GUU GAU CAA AGU CUA AUU AUU GCA GCC AGG Glu Val Arg Asn Asp Asp Val Asp Gln Ser Leu Ile Ile Ala Ala Arg 250 255 260			819
AGC AUA GUG AGA AGA GCA GCA GUA UCA GCA GAU CCA CUA GCA UCU UUA Ser Ile Val Arg Arg Ala Ala Val Ser Ala Asp Pro Leu Ala Ser Leu 265 270 275 280			867
UUG GAG AUG UGC CAC AGC ACA CAG AUU GGC GGG ACA AGG AUG GUG GAC Leu Glu Met Cys His Ser Thr Gln Ile Gly Gly Thr Arg Met Val Asp 285 290 295			915
AUU CUU AGG CAG AAC CCA ACA GAA GAG CAA GCU GUG GAA AUA UGC AAG Ile Leu Arg Gln Asn Pro Thr Glu Glu Gln Ala Val Glu Ile Cys Lys 300 305 310			963
GCU GCA AUG GGA CUG AGG AUC AGC UCA UCC UUC AGU UUU GGC GGG UUC			1011

Ala Ala Met Gly Leu Arg Ile Ser Ser Ser Phe Ser Phe Gly Gly Phe
315 320 325

ACA UUU AAG AGA ACA AGC GGA UCA UCA GUC AAG AGA GAG GAA GAA GUG
Thr Phe Lys Arg Thr Ser Gly Ser Ser Val Lys Arg Glu Glu Glu Val
330 335 340

1059

CUU ACG GGC AAU CUU CAA ACA UUG AAA AUA AGG GUG CAU GAG GGA UAC
Leu Thr Gly Asn Leu Gln Thr Leu Lys Ile Arg Val His Glu Gly Tyr
345 350 355 360

1107

GAG GAG UUC ACA AUG GUU GGG AAA AGG GCA ACA GCU AUA CUC AGA AAA
Glu Glu Phe Thr Met Val Gly Lys Arg Ala Thr Ala Ile Leu Arg Lys
365 370 375

1155

GCA ACC AGG AGA UUG AUU CAG CUG AUU GUG AGU GGA AGA GAC GAA CAG
Ala Thr Arg Arg Leu Ile Gln Leu Ile Val Ser Gly Arg Asp Glu Gln
380 385 390

1203

UCG AUA GCU GAA GCA AUA AUU GUG GCC AUG GUA UUU UCA CAA GAA GAU
Ser Ile Ala Glu Ala Ile Ile Val Ala Met Val Phe Ser Gln Glu Asp
395 400 405

1251

UGU AUG AUA AAA GCA GUU AGA GGU GAU CUG AAU UUC GUU AAU AGG GCA
Cys Met Ile Lys Ala Val Arg Gly Asp Leu Asn Phe Val Asn Arg Ala
410 415 420

1299

AAU CAG CGA UUG AAU CCC AUG CAU CAA CUU UUA AGA CAU UUU CAG AAG
Asn Gln Arg Leu Asn Pro Met His Gln Leu Leu Arg His Phe Gln Lys
425 430 435 440

1347

GAU GCG AAA GUG CUU UUU CAA AAU UGG GGA AUU GAA CAU AUC GAC AAU
Asp Ala Lys Val Leu Phe Gln Asn Trp Gly Ile Glu His Ile Asp Asn
445 450 455

1395

GUG AUG GGA AUG AUU GGG GUA UUA CCA GAC AUG ACU CCA AGC ACA GAG
Val Met Gly Met Ile Gly Val Leu Pro Asp Met Thr Pro Ser Thr Glu
460 465 470

1443

AUG UCA AUG AGA GGG GUA AGA GUC AGC AAA AUG GGC GUA GAU GAA UAC
Met Ser Met Arg Gly Val Arg Val Ser Lys Met Gly Val Asp Glu Tyr
475 480 485

1491

UCC AGC GCG GAG AGA GUA GUG GUG AGC AUU GAC CGG UUU UUG AGA GUU
Ser Ser Ala Glu Arg Val Val Val Ser Ile Asp Arg Phe Leu Arg Val
490 495 500

1539

CGA GAC CAA CGA GGA AAU GUA CUA CUA UCU CCU GAG GAG GUC AGU GAA
Arg Asp Gln Arg Gly Asn Val Leu Leu Ser Pro Glu Glu Val Ser Glu
505 510 515 520

1587

ACA CAG GGA ACA GAG AAA CUG ACA AUA ACU UAC UCA UCG UCA AUG AUG
Thr Gln Gly Thr Glu Lys Leu Thr Ile Thr Tyr Ser Ser Ser Met Met
525 530 535

1635

UGG GAG AUU AAU GGC CCU GAG UCA GUG UUG GUC AAU ACC UAU CAG UGG Trp Glu Ile Asn Gly Pro Glu Ser Val Leu Val Asn Thr Tyr Gln Trp 540 545 550	1683
AUC AUC AGA AAC UGG GAA ACU GUU AAA AUU CAG UGG UCU CAG AAU CCU Ile Ile Arg Asn Trp Glu Thr Val Lys Ile Gln Trp Ser Gln Asn Pro 555 560 565	1731
ACA AUG CUA UAC AAU AAA AUG GAA UUU GAG CCA UUU CAG UCU UUA GUU Thr Met Leu Tyr Asn Lys Met Glu Phe Glu Pro Phe Gln Ser Leu Val 570 575 580	1779
CCU AAG GCC AUU AGA GGC CAA UAC AGU GGG UUU GUU AGG ACU CUA UUC Pro Lys Ala Ile Arg Gly Gln Tyr Ser Gly Phe Val Arg Thr Leu Phe 585 590 595 600	1827
CAA CAA AUG AGG GAU GUA CUU GGG ACA UUU GAU ACC ACC CAG AUA AUA Gln Gln Met Arg Asp Val Leu Gly Thr Phe Asp Thr Thr Gln Ile Ile 605 610 615	1875
AAA CUU CUU CCC UUU GCA GCC GCC CCA CCA AAG CAA AGU AGA AUG CAG Lys Leu Leu Pro Phe Ala Ala Ala Pro Pro Lys Gln Ser Arg Met Gln 620 625 630	1923
UUC UCU UCA UUG ACU GUG AAU GUG AGG GGA UCA GGA AUG AGA AUA CUU Phe Ser Ser Leu Thr Val Asn Val Arg Gly Ser Gly Met Arg Ile Leu 635 640 645	1971
GUA AGG GGC AAU UCU CCU AUA UUC AAC UAC AAC AAG ACC ACU AAG AGA Val Arg Gly Asn Ser Pro Ile Phe Asn Tyr Asn Lys Thr Thr Lys Arg 650 655 660	2019
CUA ACA AUU CUC GGA AAG GAU GCU GGC ACU UUA ACU GAA GAC CCA GAU Leu Thr Ile Leu Gly Lys Asp Ala Gly Thr Leu Thr Glu Asp Pro Asp 665 670 675 680	2067
GAA GGC ACA UCU GGA GUG GAG UCC GCU GUU CUG AGA GGA UUC CUC AUU Glu Gly Thr Ser Gly Val Glu Ser Ala Val Leu Arg Gly Phe Leu Ile 685 690 695	2115
CUG GGC AAA GAA GAU AGG AGA UAU GGA CCA GCA UUA AGC AUC AAU GAA Leu Gly Lys Glu Asp Arg Arg Tyr Gly Pro Ala Leu Ser Ile Asn Glu 700 705 710	2163
CUG AGU AAC CUU GCG AAA GGA GAA AAG GCU AAU GUA CUA AUU GGG CAA Leu Ser Asn Leu Ala Lys Gly Glu Lys Ala Asn Val Leu Ile Gly Gln 715 720 725	2211
GGA GAC GUG GUG UUG GUA AUG AAA CGA AAA CGG AAC UCU AGC AUA CUU Gly Asp Val Val Leu Val Met Lys Arg Lys Arg Asn Ser Ser Ile Leu 730 735 740	2259
ACU GAC AGC CAG ACA GCG ACC AAA AGG AUU CGG AUG GCC AUC AAU Thr Asp Ser Gln Thr Ala Thr Lys Arg Ile Arg Met Ala Ile Asn 745 750 755	2304

UAAUGUUGAA UAGUUUAAAA ACGACCUUGU UUCUACU

2341

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Glu Arg Ile Lys Glu Leu Arg Asn Leu Met Ser Gln Ser Arg Thr
1 5 10 15

Arg Glu Ile Leu Thr Lys Thr Val Asp His Met Ala Ile Ile Lys
20 25 30

Lys Tyr Thr Ser Gly Arg Gln Glu Lys Asn Pro Ser Leu Arg Met Lys
35 40 45

Trp Met Met Ala Met Lys Tyr Pro Ile Thr Ala Asp Lys Arg Ile Thr
50 55 60

Glu Met Ile Pro Glu Arg Asn Glu Gln Gly Gln Thr Leu Trp Ser Lys
65 70 75 80

Met Ser Asp Ala Gly Ser Asp Arg Val Met Val Ser Pro Leu Ala Val
85 90 95

Thr Trp Trp Asn Arg Asn Gly Pro Met Thr Ser Thr Val His Tyr Pro
100 105 110

Lys Ile Tyr Lys Thr Tyr Phe Glu Lys Val Glu Arg Leu Lys His Gly
115 120 125

Thr Phe Gly Pro Val His Phe Arg Asn Gln Val Lys Ile Arg Arg Arg
130 135 140

Val Asp Ile Asn Pro Gly His Ala Asp Leu Ser Ala Lys Glu Ala Gln
145 150 155 160

Asp Val Ile Met Glu Val Val Phe Pro Asn Glu Val Gly Ala Arg Ile
165 170 175

Leu Thr Ser Glu Ser Gln Leu Thr Ile Thr Lys Glu Lys Lys Glu Glu
180 185 190

Leu Gln Asp Cys Lys Ile Ser Pro Leu Met Val Ala Tyr Met Leu Glu
195 200 205

Arg Glu Leu Val Arg Lys Thr Arg Phe Leu Pro Val Ala Gly Gly Thr
210 215 220

Ser Ser Val Tyr Ile Glu Val Leu His Leu Thr Gln Gly Thr Cys Trp
225 230 235 240

Glu Gln Met Tyr Thr Pro Gly Gly Glu Val Arg Asn Asp Asp Val Asp
245 250 255

Gln Ser Leu Ile Ile Ala Ala Arg Ser Ile Val Arg Arg Ala Ala Val
260 265 270

Ser Ala Asp Pro Leu Ala Ser Leu Leu Glu Met Cys His Ser Thr Gln
275 280 285

Ile Gly Gly Thr Arg Met Val Asp Ile Leu Arg Gln Asn Pro Thr Glu
290 295 300

Glu Gln Ala Val Glu Ile Cys Lys Ala Ala Met Gly Leu Arg Ile Ser
305 310 315 320

Ser Ser Phe Ser Phe Gly Gly Phe Thr Phe Lys Arg Thr Ser Gly Ser
325 330 335

Ser Val Lys Arg Glu Glu Glu Val Leu Thr Gly Asn Leu Gln Thr Leu
340 345 350

Lys Ile Arg Val His Glu Gly Tyr Glu Glu Phe Thr Met Val Gly Lys
355 360 365

Arg Ala Thr Ala Ile Leu Arg Lys Ala Thr Arg Arg Leu Ile Gln Leu
370 375 380

Ile Val Ser Gly Arg Asp Glu Gln Ser Ile Ala Glu Ala Ile Ile Val
385 390 395 400

Ala Met Val Phe Ser Gln Glu Asp Cys Met Ile Lys Ala Val Arg Gly
405 410 415

Asp Leu Asn Phe Val Asn Arg Ala Asn Gln Arg Leu Asn Pro Met His
420 425 430

Gln Leu Leu Arg His Phe Gln Lys Asp Ala Lys Val Leu Phe Gln Asn
435 440 445

Trp Gly Ile Glu His Ile Asp Asn Val Met Gly Met Ile Gly Val Leu
450 455 460

Pro Asp Met Thr Pro Ser Thr Glu Met Ser Met Arg Gly Val Arg Val
465 470 475 480

Ser Lys Met Gly Val Asp Glu Tyr Ser Ser Ala Glu Arg Val Val Val

485

490

495

Ser Ile Asp Arg Phe Leu Arg Val Arg Asp Gln Arg Gly Asn Val Leu
500 505 510

Leu Ser Pro Glu Glu Val Ser Glu Thr Gln Gly Thr Glu Lys Leu Thr
515 520 525

Ile Thr Tyr Ser Ser Met Met Trp Glu Ile Asn Gly Pro Glu Ser
530 535 540

Val Leu Val Asn Thr Tyr Gln Trp Ile Ile Arg Asn Trp Glu Thr Val
545 550 555 560

Lys Ile Gln Trp Ser Gln Asn Pro Thr Met Leu Tyr Asn Lys Met Glu
565 570 575

Phe Glu Pro Phe Gln Ser Leu Val Pro Lys Ala Ile Arg Gly Gln Tyr
580 585 590

Ser Gly Phe Val Arg Thr Leu Phe Gln Gln Met Arg Asp Val Leu Gly
595 600 605

Thr Phe Asp Thr Thr Gln Ile Ile Lys Leu Leu Pro Phe Ala Ala Ala
610 615 620

Pro Pro Lys Gln Ser Arg Met Gln Phe Ser Ser Leu Thr Val Asn Val
625 630 635 640

Arg Gly Ser Gly Met Arg Ile Leu Val Arg Gly Asn Ser Pro Ile Phe
645 650 655

Asn Tyr Asn Lys Thr Thr Lys Arg Leu Thr Ile Leu Gly Lys Asp Ala
660 665 670

Gly Thr Leu Thr Glu Asp Pro Asp Glu Gly Thr Ser Gly Val Glu Ser
675 680 685

Ala Val Leu Arg Gly Phe Leu Ile Leu Gly Lys Glu Asp Arg Arg Tyr
690 695 700

Gly Pro Ala Leu Ser Ile Asn Glu Leu Ser Asn Leu Ala Lys Gly Glu
705 710 715 720

Lys Ala Asn Val Leu Ile Gly Gln Gly Asp Val Val Leu Val Met Lys
725 730 735

Arg Lys Arg Asn Ser Ser Ile Leu Thr Asp Ser Gln Thr Ala Thr Lys
740 745 750

Arg Ile Arg Met Ala Ile Asn
755

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PB1

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(123, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(486, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3); c in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1195, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(1276, "a")

(D) OTHER INFORMATION: /note= "g in ca "master" strain; a in wt2(3); g in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1395, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3); g in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1766, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(2005, "a")

(D) OTHER INFORMATION: /note= "a in ca "master" strain and in wt2(3); g in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- a\
- (A) NAME/KEY: conflict
 - (B) LOCATION: replace(2019, "u")
 - (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3); c in 1988 reported wild type E28-32 strain"
/citation= ([1] [2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 25..2295
- (D) OTHER INFORMATION: /product= "polymerase basic 1"
/gene= "PB1"
/note= "polymerase basic 1"
/citation= ([1] [2])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
- (B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) influenza virus
- (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
- (G) DATE: 1993
- (K) RELEVANT RESIDUES IN SEQ ID NO:31: FROM 1 TO 2341

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C
- (B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza vaccine strain
- (C) JOURNAL: Virology
- (D) VOLUME: 167
- (F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:31: FROM 1 TO 2341

a/

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:				
AGCGAAAGCA	GGCAAACCAU	UUGA	AUG	51
Met	Asp	Val	Asn	
1	5			
UUG	AAA	GUU	CCA	99
CYT	VAL	PRO	ALA	
10	15	20	25	
GGA	GAU	CCU	CCA	147
Gly	Asp	Pro	Pro	
30	35	40		
ACA	GUC	AAC	AGA	195
Thr	Val	Asn	Arg	
45	50	55		
AAC	ACG	GAA	ACU	243
Asn	Thr	Glu	Thr	
60	65	70		
CCU	GAG	GAC	AAU	291
Pro	Glu	Asp	Asn	
75	80	85		
GAA	GCA	AUG	GCU	339
Glu	Ala	Met	Ala	
90	95	100	105	
UCG	UGU	CUU	GAA	387
Ser	Cys	Leu	Glu	
110	115	120		
CUG	ACC	CAA	GGU	435
Leu	Thr	Gln	Gly	
125	130	135		
CCG	GCU	GCA	ACU	483
Pro	Ala	Ala	Thr	
140	145	150		
GGU	CUG	ACA	GCU	531
Gly	Leu	Thr	Ala	
155	160	165		
GUG	AUA	GAA	UCA	579
Val	Ile	Glu	Ser	
170	175	180	185	

CAA AGA AAA AGA AGA GUA AGA GAC AAC AUG ACC AAG AAA AUG GUC ACA Gln Arg Lys Arg Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr 190 195 200	627
CAA CGA ACA AUA GGA AAG AAG CAA AGA UUG AAC AAG AGA AGC UAU Gln Arg Thr Ile Gly Lys Lys Gln Arg Leu Asn Lys Arg Ser Tyr 205 210 215	675
CUA AUA AGA GCA CUG ACA UUG AAC ACA AUG ACU AAA GAU GCA GAG AGA Leu Ile Arg Ala Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg 220 225 230	723
GGU AAA UUA AAG AGA AGA GCA AUU GCA ACA CCC GGU AUG CAG AUC AGA Gly Lys Leu Lys Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg 235 240 245	771
GGG UUC GUG UAC UUU GUC GAA ACA CUA GCG AGA AGU AUU UGU GAG AAG Gly Phe Val Tyr Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys 250 255 260 265	819
CUU GAA CAG UCU GGG CUU CCG GUU GGA GGU AAU GAA AAG AAG GCU AAA Leu Glu Gln Ser Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys 270 275 280	867
CUG GCA AAU GUU GUG CGA AAA AUG AUG ACU AAU UCA CAA GAC ACA GAG Leu Ala Asn Val Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu 285 290 295	915
CUC UCU UUC ACA AUU ACU GGA GAC AAU ACC AAA UGG AAU GAG AAU CAA Leu Ser Phe Thr Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln 300 305 310	963
AAU CCU CGG AUG UUC CUG GCG AUG AUA ACA UAC AUC ACA AGA AAU CAA Asn Pro Arg Met Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln 315 320 325	1011
CCU GAA UGG UUU AGA AAC GUC CUG AGC AUC GCA CCU AUA AUG UUC UCA Pro Glu Trp Phe Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser 330 335 340 345	1059
AAU AAA AUG GCA AGA CUA GGG AAA GGA UAC AUG UUC AAA AGC AAG AGC Asn Lys Met Ala Arg Leu Gly Lys Gly Tyr Met Phe Lys Ser Lys Ser 350 355 360	1107
AUG AAG CUC CGA ACA CAA AUA CCA GCA GAA AUG CUA GCA AGU AUU GAC Met Lys Leu Arg Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp 365 370 375	1155
CUG AAA UAC UUU AAU GAA UCA ACA AGA AAG AAA AUC GAG GAA AUA AGG Leu Lys Tyr Phe Asn Glu Ser Thr Arg Lys Lys Ile Glu Glu Ile Arg 380 385 390	1203
CCU CUC CUA AUA GAU GGC ACA GUC UCA UUG AGU CCU GGA AUG AUG AUG Pro Leu Leu Ile Asp Gly Thr Val Ser Leu Ser Pro Gly Met Met Met 395 400 405	1251

GGC AUG UUC AAC AUG CUA AGU ACA AUC UUA GGA GUC UCA AUC CUG AAU Gly Met Phe Asn Met Leu Ser Thr Ile Leu Gly Val Ser Ile Leu Asn 410 415 420 425	1299
CUU GGA CAA AAG AAG UAC ACC AAA ACA ACA UAC UGG UGG GAC GGA CUC Leu Gly Gln Lys Lys Tyr Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu 430 435 440	1347
CAA UCC UCU GAU GAC UUC GCC CUC AUA GUG AAU GCA CCA AAU CAU GAU Gln Ser Ser Asp Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Asp 445 450 455	1395
GGA AUA CAA GCA GGG GUG GAU AGA UUC UAC AGA ACC UGC AAG CUA GUC Gly Ile Gln Ala Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val 460 465 470	1443
GGA AUC AAU AUG AGC AAA AAG AAG UCC UAC AUA AAU AGG ACA GGG ACA Gly Ile Asn Met Ser Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr 475 480 485	1491
UUU GAA UUC ACA AGC UUU UUC UAU CGC UAU GGA UUU GUA GCC AAU UUU Phe Glu Phe Thr Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe 490 495 500 505	1539
AGC AUG GAG CUG CCC AGC UUU GGA GUG UCU GGA AUU AAU GAA UCG GCU Ser Met Glu Leu Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala 510 515 520	1587
GAU AUG AGC AUU GGG GUA ACA GUG AUA AAG AAC AAC AUG AUA AAC AAU Asp Met Ser Ile Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn 525 530 535	1635
GAC CUU GGG CCA GCA ACA GCC CAA CUG GCU CUU CAA CUA UUC AUC AAA Asp Leu Gly Pro Ala Thr Ala Gln Leu Ala Leu Gln Leu Phe Ile Lys 540 545 550	1683
GAC UAC AGA UAU ACG UAC CGG UGC CAC AGA GGA GAC ACA CAA AUU CAG Asp Tyr Arg Tyr Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln 555 560 565	1731
ACA AGG AGA UCA UUC GAG CUA AAG AAG CUG UGG GGG CAA ACC ACC CGC UCA Thr Arg Arg Ser Phe Glu Leu Lys Lys Leu Trp Gly Gln Thr Arg Ser 570 575 580 585	1779
AAG GCA GGA CUU UUG GUU UCG GAU GGA GGA CCA AAC UUA UAC AAU AUC Lys Ala Gly Leu Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile 590 595 600	1827
CGG AAU CUC CAC AUU CCA GAA GUC UGC UUG AAG UGG GAG CUA AUG GAU Arg Asn Leu His Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp 605 610 615	1875
GAA GAC UAU CAG GGG AGG CUU UGU AAU CCC CUG AAU CCA UUU GUC AGU Glu Asp Tyr Gln Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Ser 620 625 630	1923

CAU AAG GAG AUU GAG UCU GUA AAC AAU GCU GUG GUA AUG CCA GCU CAC 1971
His Lys Glu Ile Glu Ser Val Asn Asn Ala Val Val Met Pro Ala His
635 640 645

GGU CCA GCC AAG AGC AUG GAA UAU GAU GCU GUU ACU ACU ACA CAC UCU 2019
Gly Pro Ala Lys Ser Met Glu Tyr Asp Ala Val Thr Thr Thr His Ser
650 655 660 665

UGG AUC CCU AAG AGG AAC CGC UCC AUU CUC AAC ACA AGC CAA AGG GGA 2067
Trp Ile Pro Lys Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly
670 675 680

AUU CUU GAA GAU GAA CAG AUG UAU CAG AAG UGU UGC AAU CUA UUC GAG 2115
Ile Leu Glu Asp Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu
685 690 695

AAA UUC UUC CCU AGC AGU UCG UAC AGG AGA CCA GUU GGA AUU UCC AGC 2163
Lys Phe Phe Pro Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser
700 705 710

AUG GUG GAG GCC AUG GUG UCU AGG GCC CGG AUU GAU GCA CGG AUU GAC 2211
Met Val Glu Ala Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp
715 720 725

UUC GAG UCU GGA CGG AUU AAG AAA GAG GAG UUC GCU GAG AUC AUG AAG 2259
Phe Glu Ser Gly Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys
730 735 740 745

AUC UGU UCC ACC AUU GAA GAG CUC AGA CGG CAA AAA UAGUGAAUUU 2305
Ile Cys Ser Thr Ile Glu Glu Leu Arg Arg Gln Lys
750 755

AGCUUGUCCU UCAUGAAAAA AUGCCUUGUU UCUACU 2341

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn
1 5 10 15

Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His

20

25

30

Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
35 40 45

Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr Gly Ala His
50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
85 90 95

Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu Thr Met Glu
100 105 110

Val Ile Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
130 135 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
145 150 155 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Ile Glu Ser Met Asp Lys
165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Lys
195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
210 215 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
225 230 235 240

Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
245 250 255

Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
260 265 270

Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
275 280 285

Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
290 295 300

Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
305 310 315 320

Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
325 330 335

Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
340 345 350

Lys Gly Tyr Met Phe Lys Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
355 360 365

Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Ser
370 375 380

Thr Arg Lys Lys Ile Glu Glu Ile Arg Pro Leu Leu Ile Asp Gly Thr
385 390 395 400

Val Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
405 410 415

Thr Ile Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Lys Tyr Thr
420 425 430

Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
435 440 445

Leu Ile Val Asn Ala Pro Asn His Asp Gly Ile Gln Ala Gly Val Asp
450 455 460

Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
465 470 475 480

Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
485 490 495

Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
500 505 510

Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
515 520 525

Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
530 535 540

Gln Leu Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
545 550 555 560

Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
565 570 575

Lys Lys Leu Trp Gly Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
580 585 590

Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
595 600 605

Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu

610 615 620
Cys Asn Pro Leu Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
625 630 635 640
a)
Asn Asn Ala Val Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
645 650 655
Tyr Asp Ala Val Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
660 665 670
Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
675 680 685
Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
690 695 700
Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
705 710 715 720
Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
725 730 735
Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
740 745 750
Leu Arg Arg Gln Lys
755

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

(B) CLONE: PA

a\ (ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(20, "c")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain and in wt2(3); u in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(75, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); u in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1861, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(2167..2168, "cc")
- (D) OTHER INFORMATION: /note= "cc in ca "master" strain and in wt2(3); uu in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 25..2172

(D) OTHER INFORMATION: /product= "polymerase acidic protein"
/gene= "PA"
/note= "polymerase acidic protein"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:33: FROM 1 TO 2233

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza strain, A/Ann Arbor/6/60(H2N2)

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:33: FROM 1 TO 2233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGCGAAAGCA GGUACUGAUC CGAA AUG GAA GAU UUU GUG CGA CAA UGC UUC
Met Glu Asp Phe Val Arg Gln Cys Phe
1 5

51

AAU CCG AUG AUU GUC GAG CUU GCG GAA AAA GCA AUG AAA GAG UAU GGA

99

Asn Pro Met Ile Val Glu Leu Ala Glu Lys Ala Met Lys Glu Tyr Gly
10 15 20 25

GAG GAU CUG AAA AUC GAA ACA AAC AAA UUU GCA GCA AUA UGC ACU CAC
Glu Asp Leu Lys Ile Glu Thr Asn Lys Phe Ala Ala Ile Cys Thr His
30 35 40

147

UUG GAA GUA UGC UUC AUG UAU UCA GAU UUU CAU UUC AUC AAU GAG CAA
Leu Glu Val Cys Phe Met Tyr Ser Asp Phe His Phe Ile Asn Glu Gln
45 50 55

195

GGC GAG UCA AUA AUA GUA GAG CUU GAU GAU CCA AAU GCA CUU UUG AAG
Gly Glu Ser Ile Ile Val Glu Leu Asp Asp Pro Asn Ala Leu Leu Lys
60 65 70

243

CAC AGA UUU GAA AUA AUA GAG GGA AGA GAU CGC ACA AUG GCC UGG ACA
His Arg Phe Glu Ile Ile Glu Gly Arg Asp Arg Thr Met Ala Trp Thr
75 80 85

291

GUA GUA AAC AGU AUU UGC AAC ACU ACA GGA GCU GAG AAA CCG AAG UUU
Val Val Asn Ser Ile Cys Asn Thr Thr Gly Ala Glu Lys Pro Lys Phe
90 95 100 105

339

CUG CCA GAU UUG UAU GAU UAC AAG GAG AAU AGA UUC AUC GAG AUU GGA
Leu Pro Asp Leu Tyr Asp Tyr Lys Glu Asn Arg Phe Ile Glu Ile Gly
110 115 120

387

GUG ACA AGG AGG GAA GUC CAC AUA UAC UAU CUU GAA AAG GCC AAU AAA
Val Thr Arg Arg Glu Val His Ile Tyr Tyr Leu Glu Lys Ala Asn Lys
125 130 135

435

AUU AAA UCU GAG AAG ACA CAC AUC CAC AUU UUC UCA UUC ACU GGG GAA
Ile Lys Ser Glu Lys Thr His Ile His Ile Phe Ser Phe Thr Gly Glu
140 145 150

483

GAA AUG GCC ACA AAG GCC GAC UAC ACU CUC GAU GAG GAA AGC AGG GCU
Glu Met Ala Thr Lys Ala Asp Tyr Thr Leu Asp Glu Glu Ser Arg Ala
155 160 165

531

AGG AUC AAA ACC AGA CUA UUC ACC AUA AGA CAA GAA AUG GCU AGC AGA
Arg Ile Lys Thr Arg Leu Phe Thr Ile Arg Gln Glu Met Ala Ser Arg
170 175 180 185

579

GGC CUC UGG GAU UCC UUU CAU CAG UCC GAA AGA GGC GAA GAA ACA AUU
Gly Leu Trp Asp Ser Phe His Gln Ser Glu Arg Gly Glu Glu Thr Ile
190 195 200

627

GAA GAA AGA UUU GAA AUC ACA GGG ACA AUG CGC AGG CUC GCC GAC CAA
Glu Glu Arg Phe Glu Ile Thr Gly Thr Met Arg Arg Leu Ala Asp Gln
205 210 215

675

AGU CUC CCG CCG AAC UUC UCC UGC CUU GAG AAU UUU AGA GCC UAU GUG
Ser Leu Pro Pro Asn Phe Ser Cys Leu Glu Asn Phe Arg Ala Tyr Val
220 225 230

723

GAU GGA UUC GAA CCG AAC GGC UAC AUU GAG GGC AAG CUU UCU CAA AUG Asp Gly Phe Glu Pro Asn Gly Tyr Ile Glu Gly Lys Leu Ser Gln Met 235 240 245	771
UCC AAA GAA GUA AAU GCU AAA AUU GAA CCU UUU CUG AAA ACA ACA CCA Ser Lys Glu Val Asn Ala Lys Ile Glu Pro Phe Leu Lys Thr Thr Pro 250 255 260 265	819
AGA CCA AUU AGA CUU CCG GAU GGG CCU CCU UGU UCU CAG CGG UCC AAA Arg Pro Ile Arg Leu Pro Asp Gly Pro Pro Cys Ser Gln Arg Ser Lys 270 275 280	867
UUC CUG CUG AUG GAU GCU UUA AAA UUA AGC AUU GAG GAC CCA AGU CAC Phe Leu Leu Met Asp Ala Leu Lys Leu Ser Ile Glu Asp Pro Ser His 285 290 295	915
GAA GGA GAG GGA AUA CCA CUA UAU GAU GCG AUC AAG UGU AUG AGA ACA Glu Gly Glu Gly Ile Pro Leu Tyr Asp Ala Ile Lys Cys Met Arg Thr 300 305 310	963
UUC UUU GGA UGG AAA GAA CCC UAU GUU GUU AAA CCA CAC GAA AAG GGA Phe Phe Gly Trp Lys Glu Pro Tyr Val Val Lys Pro His Glu Lys Gly 315 320 325	1011
AUA AAU CCA AAU UAU CUG CUG UCA UGG AAG CAA GUA CUG GCA GAA CUG Ile Asn Pro Asn Tyr Leu Leu Ser Trp Lys Gln Val Leu Ala Glu Leu 330 335 340 345	1059
CAG GAC AUU GAG AAU GAG GAG AAG AUU CCA AGA ACC AAA AAC AUG AAG Gln Asp Ile Glu Asn Glu Glu Lys Ile Pro Arg Thr Lys Asn Met Lys 350 355 360	1107
AAA ACG AGU CAG CUA AAG UGG GCA CUU GGU GAG AAC AUG GCA CCA GAG Lys Thr Ser Gln Leu Lys Trp Ala Leu Gly Glu Asn Met Ala Pro Glu 365 370 375	1155
AAG GUU GAC UUU GAC GAC UGU AGA GAU GUA AGC GAU UUG AAG CAA UAU Lys Val Asp Phe Asp Asp Cys Arg Asp Val Ser Asp Leu Lys Gln Tyr 380 385 390	1203
GAU AGU GAU GAA CCU GAA UUA AGG UCA CUU UCA AGC UGG AUC CAG AAU Asp Ser Asp Glu Pro Glu Leu Arg Ser Leu Ser Ser Trp Ile Gln Asn 395 400 405	1251
GAG UUC AAC AAG GCA UGC GAG CUG ACC GAU UCA AUC UGG AUA GAG CUC Glu Phe Asn Lys Ala Cys Glu Leu Thr Asp Ser Ile Trp Ile Glu Leu 410 415 420 425	1299
GAU GAG AUU GGA GAA GAU GUG GCU CCA AUU GAA CAC AUU GCA AGC AUG Asp Glu Ile Gly Glu Asp Val Ala Pro Ile Glu His Ile Ala Ser Met 430 435 440	1347
AGA AGG AAU UAC UUC ACA GCA GAG GUG UCU CAU UGC AGA GCC ACA GAA Arg Arg Asn Tyr Phe Thr Ala Glu Val Ser His Cys Arg Ala Thr Glu 445 450 455	1395

UAU AUA AUG AAG GGG GUA UAC AUU AAU ACU GCC UUG CUU AAU GCA UCC Tyr Ile Met Lys Gly Val Tyr Ile Asn Thr Ala Leu Leu Asn Ala Ser 460 465 470	1443
UGU GCA GCA AUG GAC GAU UUC CAA CUA AUU CCC AUG AUA AGC AAA UGU Cys Ala Ala Met Asp Asp Phe Gln Leu Ile Pro Met Ile Ser Lys Cys 475 480 485	1491
AGA ACU AAA GAG GGA AGG CGA AAG ACC AAU UUA UAU GGU UUC AUC AUA Arg Thr Lys Glu Gly Arg Arg Lys Thr Asn Leu Tyr Gly Phe Ile Ile 490 495 500 505	1539
AAA GGA AGA UCU CAC UUA AGG AAU GAC ACC GAC GUG GUA AAC UUU GUG Lys Gly Arg Ser His Leu Arg Asn Asp Thr Asp Val Val Asn Phe Val 510 515 520	1587
AGC AUG GAG UUU UCU CUC ACU GAC CCA AGA CUU GAG CCA CAC AAA UGG Ser Met Glu Phe Ser Leu Thr Asp Pro Arg Leu Glu Pro His Lys Trp 525 530 535	1635
GAG AAG UAC UGU GUU CUU GAG AUA GGA GAU AUG CUA CUA AGA AGU GCC Glu Lys Tyr Cys Val Leu Glu Ile Gly Asp Met Leu Leu Arg Ser Ala 540 545 550	1683
AUA GGC CAG GUG UCA AGG CCC AUG UUC UUG UAU GUG AGG ACA AAU GGA Ile Gly Gln Val Ser Arg Pro Met Phe Leu Tyr Val Arg Thr Asn Gly 555 560 565	1731
ACA UCA AAG AUU AAA AUG AAA UGG GGA AUG GAG AUG AGG CGU UGC CUC Thr Ser Lys Ile Lys Met Lys Trp Gly Met Glu Met Arg Arg Cys Leu 570 575 580 585	1779
CUU CAG UCA CUC CAA CAA AUC GAG AGU AUG AUU GAA GCC GAG UCC UCU Leu Gln Ser Leu Gln Gln Ile Glu Ser Met Ile Glu Ala Glu Ser Ser 590 595 600	1827
GUC AAG GAG AAA GAC AUG ACC AAA GAG UUU UUC GAG AAU AAA UCA GAA Val Lys Glu Lys Asp Met Thr Lys Glu Phe Phe Glu Asn Lys Ser Glu 605 610 615	1875
ACA UGG CCC AUU GGA GAG UCC CCC AAA GGA GUG GAA GAA GGU UCC AUU Thr Trp Pro Ile Gly Glu Ser Pro Lys Gly Val Glu Glu Gly Ser Ile 620 625 630	1923
GGG AAG GUC UGC AGG ACU UUA UUA GCC AAG UCG GUA UUC AAU AGC CUG Gly Lys Val Cys Arg Thr Leu Leu Ala Lys Ser Val Phe Asn Ser Leu 635 640 645	1971
UAU GCA UCU CCA CAA UUA GAA GGA UUU UCA GCU GAA UCA AGA AAA CUG Tyr Ala Ser Pro Gln Leu Glu Gly Phe Ser Ala Glu Ser Arg Lys Leu 650 655 660 665	2019
CUU CUU GUC GUU CAG GCU CUU AGG GAC AAU CUU GAA CCU GGG ACC UUU Leu Leu Val Val Gln Ala Leu Arg Asp Asn Leu Glu Pro Gly Thr Phe 670 675 680	2067

GAU CUU GGG GGG CUA UAU GAA GCA AUU GAG GAG UGC CUG AUU AAU GAU 2115
Asp Leu Gly Gly Leu Tyr Glu Ala Ile Glu Glu Cys Leu Ile Asn Asp
685 690 695

CCC UGG GUU UUG CUU AAU GCG UCU UGG UUC AAC UCC UUC CUA ACA CAU 2163
Pro Trp Val Leu Leu Asn Ala Ser Trp Phe Asn Ser Phe Leu Thr His
700 705 710

GCA CCA AGA UAGUUGUGGC AAUGCUACUA UUUGCUAUCC AUACUGUCCA 2212
Ala Pro Arg
715

AAAAAGUACC UUGUUUCUAC U 2233

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Glu Asp Phe Val Arg Gln Cys Phe Asn Pro Met Ile Val Glu Leu
1 5 10 15

Ala Glu Lys Ala Met Lys Glu Tyr Gly Glu Asp Leu Lys Ile Glu Thr
20 25 30

Asn Lys Phe Ala Ala Ile Cys Thr His Leu Glu Val Cys Phe Met Tyr
35 40 45

Ser Asp Phe His Phe Ile Asn Glu Gln Gly Glu Ser Ile Ile Val Glu
50 55 60

Leu Asp Asp Pro Asn Ala Leu Leu Lys His Arg Phe Glu Ile Ile Glu
65 70 75 80

Gly Arg Asp Arg Thr Met Ala Trp Thr Val Val Asn Ser Ile Cys Asn
85 90 95

Thr Thr Gly Ala Glu Lys Pro Lys Phe Leu Pro Asp Leu Tyr Asp Tyr
100 105 110

Lys Glu Asn Arg Phe Ile Glu Ile Gly Val Thr Arg Arg Glu Val His
115 120 125

Ile Tyr Tyr Leu Glu Lys Ala Asn Lys Ile Lys Ser Glu Lys Thr His
130 135 140

Ile His Ile Phe Ser Phe Thr Gly Glu Glu Met Ala Thr Lys Ala Asp
145 150 155 160

Tyr Thr Leu Asp Glu Glu Ser Arg Ala Arg Ile Lys Thr Arg Leu Phe
165 170 175

Thr Ile Arg Gln Glu Met Ala Ser Arg Gly Leu Trp Asp Ser Phe His
180 185 190

Gln Ser Glu Arg Gly Glu Glu Thr Ile Glu Glu Arg Phe Glu Ile Thr
195 200 205

Gly Thr Met Arg Arg Leu Ala Asp Gln Ser Leu Pro Pro Asn Phe Ser
210 215 220

Cys Leu Glu Asn Phe Arg Ala Tyr Val Asp Gly Phe Glu Pro Asn Gly
225 230 235 240

Tyr Ile Glu Gly Lys Leu Ser Gln Met Ser Lys Glu Val Asn Ala Lys
245 250 255

Ile Glu Pro Phe Leu Lys Thr Thr Pro Arg Pro Ile Arg Leu Pro Asp
260 265 270

Gly Pro Pro Cys Ser Gln Arg Ser Lys Phe Leu Leu Met Asp Ala Leu
275 280 285

Lys Leu Ser Ile Glu Asp Pro Ser His Glu Gly Glu Gly Ile Pro Leu
290 295 300

Tyr Asp Ala Ile Lys Cys Met Arg Thr Phe Phe Gly Trp Lys Glu Pro
305 310 315 320

Tyr Val Val Lys Pro His Glu Lys Gly Ile Asn Pro Asn Tyr Leu Leu
325 330 335

Ser Trp Lys Gln Val Leu Ala Glu Leu Gln Asp Ile Glu Asn Glu Glu
340 345 350

Lys Ile Pro Arg Thr Lys Asn Met Lys Lys Thr Ser Gln Leu Lys Trp
355 360 365

Ala Leu Gly Glu Asn Met Ala Pro Glu Lys Val Asp Phe Asp Asp Cys
370 375 380

Arg Asp Val Ser Asp Leu Lys Gln Tyr Asp Ser Asp Glu Pro Glu Leu
385 390 395 400

Arg Ser Leu Ser Ser Trp Ile Gln Asn Glu Phe Asn Lys Ala Cys Glu
405 410 415

Leu Thr Asp Ser Ile Trp Ile Glu Leu Asp Glu Ile Gly Glu Asp Val

420

425

430

Ala Pro Ile Glu His Ile Ala Ser Met Arg Arg Asn Tyr Phe Thr Ala
435 440 445

Glu Val Ser His Cys Arg Ala Thr Glu Tyr Ile Met Lys Gly Val Tyr
450 455 460

Ile Asn Thr Ala Leu Leu Asn Ala Ser Cys Ala Ala Met Asp Asp Phe
465 470 475 480

Gln Leu Ile Pro Met Ile Ser Lys Cys Arg Thr Lys Glu Gly Arg Arg
485 490 495

Lys Thr Asn Leu Tyr Gly Phe Ile Ile Lys Gly Arg Ser His Leu Arg
500 505 510

Asn Asp Thr Asp Val Val Asn Phe Val Ser Met Glu Phe Ser Leu Thr
515 520 525

Asp Pro Arg Leu Glu Pro His Lys Trp Glu Lys Tyr Cys Val Leu Glu
530 535 540

Ile Gly Asp Met Leu Leu Arg Ser Ala Ile Gly Gln Val Ser Arg Pro
545 550 555 560

Met Phe Leu Tyr Val Arg Thr Asn Gly Thr Ser Lys Ile Lys Met Lys
565 570 575

Trp Gly Met Glu Met Arg Arg Cys Leu Leu Gln Ser Leu Gln Gln Ile
580 585 590

Glu Ser Met Ile Glu Ala Glu Ser Ser Val Lys Glu Lys Asp Met Thr
595 600 605

Lys Glu Phe Phe Glu Asn Lys Ser Glu Thr Trp Pro Ile Gly Glu Ser
610 615 620

Pro Lys Gly Val Glu Glu Gly Ser Ile Gly Lys Val Cys Arg Thr Leu
625 630 635 640

Leu Ala Lys Ser Val Phe Asn Ser Leu Tyr Ala Ser Pro Gln Leu Glu
645 650 655

Gly Phe Ser Ala Glu Ser Arg Lys Leu Leu Leu Val Val Gln Ala Leu
660 665 670

Arg Asp Asn Leu Glu Pro Gly Thr Phe Asp Leu Gly Leu Tyr Glu
675 680 685

Ala Ile Glu Glu Cys Leu Ile Asn Asp Pro Trp Val Leu Leu Asn Ala
690 695 700

Ser Trp Phe Asn Ser Phe Leu Thr His Ala Pro Arg
705 710 715

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HA

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(144, "a")
- (D) OTHER INFORMATION: /gene= "HA"
/note= "u in ca "master" strain; a in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(455, "g")
- (D) OTHER INFORMATION: /gene= "HA"
/note= "a in ca "master" strain; g in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

- (A) NAME/KEY: mutation

- (B) LOCATION: replace(729, "a")
(D) OTHER INFORMATION: /gene= "HA"
/note= "c in ca "master" strain; a in
wt2(3)"
/citation= ([1])

a
(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 44..1729
(D) OTHER INFORMATION: /product= "hemagglutinin"
/gene= "HA"
/note= "hemagglutinin protein"
/citation= ([1])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
(B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) influenza virus
(C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA
(G) DATE: 1993
(K) RELEVANT RESIDUES IN SEQ ID NO:35: FROM 1 TO 1773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGCAAAAGCA GGGGUUAUAC CAUAGACAAC CAAAAGCAAA ACA AUG GCC AUC AUU Met Ala Ile Ile	55
1	
UAU CUC AUU CUC CUG UUC ACA GCA GUG AGA GGG GAC AAG AUA UGC AUU Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Asp Lys Ile Cys Ile	103
5 10 15 20	
GGA UAC CAU GCC AAU AAU UCC ACA GAG ACG GUC GAC ACA AAU CUA GAG Gly Tyr His Ala Asn Asn Ser Thr Glu Thr Val Asp Thr Asn Leu Glu	151
25 30 35	
CGG AAC GUC ACU GUG ACU CAU GCC AAG GAC AUU CUU GAG AAG ACC CAU Arg Asn Val Thr Val Thr His Ala Lys Asp Ile Leu Glu Lys Thr His	199
40 45 50	

AAC GGA AAG UUA UGC AAA CUA AAC GGA AUC CCU CCA CUU GAA CUA GGG Asn Gly Lys Leu Cys Lys Leu Asn Gly Ile Pro Pro Leu Glu Leu Gly 55 60 65	247
GAC UGU AGC AUU GCC GGA UGG CUC CUU GGA AAU CCA GAA UGU GAU AGG Asp Cys Ser Ile Ala Gly Trp Leu Leu Gly Asn Pro Glu Cys Asp Arg 70 75 80	295
CUU CUA AGU GUG CCA GAA UGG UCC UAU AUA AUG GAG AAA GAA AAC CCG Leu Leu Ser Val Pro Glu Trp Ser Tyr Ile Met Glu Lys Glu Asn Pro 85 90 95 100	343
AGA AAC GGU UUG UGU UAU CCA GGC AAC UUC AAU GAU UAU GAA GAA UUG Arg Asn Gly Leu Cys Tyr Pro Gly Asn Phe Asn Asp Tyr Glu Glu Leu 105 110 115	391
AAA CAU CUC CUC AGC AGC GUG AAA CAU UUC GAG AAA GUA AAG AUU CUG Lys His Leu Leu Ser Ser Val Lys His Phe Glu Lys Val Lys Ile Leu 120 125 130	439
CCC AAA GAU AGA UGG GCA CAG CAU ACA ACA ACU GGA GGU UCA CAG GCC Pro Lys Asp Arg Trp Ala Gln His Thr Thr Thr Gly Gly Ser Gln Ala 135 140 145	487
UGC GCG GUG UCU GGU AAU CCA UCA UUC UUC AGG AAC AUG GUC UGG CUG Cys Ala Val Ser Gly Asn Pro Ser Phe Phe Arg Asn Met Val Trp Leu 150 155 160	535
ACA GAG GAA GGA UCA AAU UAU CCG GUU GCC AAA GGA UCG UAC AAC AAU Thr Glu Glu Gly Ser Asn Tyr Pro Val Ala Lys Gly Ser Tyr Asn Asn 165 170 175 180	583
ACA AGC GGA GAA CAA AUG CUA AUA AUU UGG GGG GUG CAC CAU CCC AUU Thr Ser Gly Glu Gln Met Leu Ile Ile Trp Gly Val His His Pro Ile 185 190 195	631
GAU GAG ACA GAA CAA AGA ACA UUG UAC CAG AAU GUG GGA ACC UAU GUU Asp Glu Thr Glu Gln Arg Thr Leu Tyr Gln Asn Val Gly Thr Tyr Val 200 205 210	679
UCC GUA GGC ACA UCA ACA UUG AAC AAA AGG UCA ACC CCA GAA AUA GCA Ser Val Gly Thr Ser Thr Leu Asn Lys Arg Ser Thr Pro Glu Ile Ala 215 220 225	727
AAA AGG CCU AAA GUG AAU GGA CUA GGA AGU AGA AUG GAA UUC UCU UGG Lys Arg Pro Lys Val Asn Gly Leu Gly Ser Arg Met Glu Phe Ser Trp 230 235 240	775
ACC CUC UUG GAU AUG UGG GAC ACC AUA AAU UUU GAG AGU ACU GGU AAU Thr Leu Leu Asp Met Trp Asp Thr Ile Asn Phe Glu Ser Thr Gly Asn 245 250 255 260	823
CUA AUU GCA CCA GAG UAU GGA UUC AAA AUA UCG AAA AGA GGU AGU UCU Leu Ile Ala Pro Glu Tyr Gly Phe Lys Ile Ser Lys Arg Gly Ser Ser 265 270 275	871

GGG AUC AUG AAA ACA GAA GGA ACA CUU GAG AAC UGU GAG ACC AAA UGC Gly Ile Met Lys Thr Glu Gly Thr Leu Glu Asn Cys Glu Thr Lys Cys 280 285 290	919
CAA ACU CCU UUG GGA GCA AUA AAU ACA ACA UUG CCU UUU CAC AAU GUC Gln Thr Pro Leu Gly Ala Ile Asn Thr Thr Leu Pro Phe His Asn Val 295 300 305	967
CAC CCA CUG ACA AUA GGU GAG UGC CCC AAA UAU GUA AAA UCG GAG AAG His Pro Leu Thr Ile Gly Glu Cys Pro Lys Tyr Val Lys Ser Glu Lys 310 315 320	1015
UUG GUC UUA GCA ACA GGA CUA AGG AAU GUU CCC CAG AUU GAA UCA AGA Leu Val Leu Ala Thr Gly Leu Arg Asn Val Pro Gln Ile Glu Ser Arg 325 330 335 340	1063
GGA UUG UUU GGG GCA AUA GCU GGU UUU AUA GAA GGA GGA UGG CAA GGA Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly 345 350 355	1111
AUG GUU GAU GGU UGG UAU GGA UAC CAU CAC AGC AAU GAC CAG GGA UCA Met Val Asp Gly Trp Tyr Gly Tyr His His Ser Asn Asp Gln Gly Ser 360 365 370	1159
GGG UAU GCA GCA GAC AAA GAA UCC ACU CAA AAG GCA UUU GAU GGA AUC Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala Phe Asp Gly Ile 375 380 385	1207
ACC AAC AAG GUA AAU UCU GUG AUU GAA AAG AUA AAC ACC CAA UUU GAA Thr Asn Lys Val Asn Ser Val Ile Glu Lys Ile Asn Thr Gln Phe Glu 390 395 400	1255
GCU GUU GGG AAA GAA UUC AGU AAC UUA GAG AGA AGA CUG GAG AAC UUG Ala Val Gly Lys Glu Phe Ser Asn Leu Glu Arg Arg Leu Glu Asn Leu 405 410 415 420	1303
AAC AAA AAG AUG GAA GAC GGG UUU CUA GAU GUG UGG ACA UAC AAU GCU Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala 425 430 435	1351
GAG CUU CUA GUU CUG AUG GAA AAU GAG AGG ACA CUU GAC UUU CAU GAU Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu Asp Phe His Asp 440 445 450	1399
UCU AAU GUC AAG AAU CUG UAU GAU AAA GUC AGA AUG CAG CUG AGG GAC Ser Asn Val Lys Asn Leu Tyr Asp Lys Val Arg Met Gln Leu Arg Asp 455 460 465	1447
AAC GUC AAA GAA CUA GGA AAU GGA UGU UUU GAA UUU UAU CAC AAA UGU Asn Val Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe Tyr His Lys Cys 470 475 480	1495
GAU GAU GAA UGC AUG AAU AGU GUG AAA AAC GGG ACA UAU GAU UAU CCC Asp Asp Glu Cys Met Asn Ser Val Lys Asn Gly Thr Tyr Asp Tyr Pro 485 490 495 500	1543

AAG UAU GAA GAA GAG UCU AAA CUA AAU AGA AAU GAA AUU AAA GGG GUA Lys Tyr Glu Glu Glu Ser Lys Leu Asn Arg Asn Glu Ile Lys Gly Val 505 510 515	1591
AAA UUG AGC AGC AUG GGG GUU UGU CGG AUC CUU GCC AUU UAU GCU ACA Lys Leu Ser Ser Met Gly Val Cys Arg Ile Leu Ala Ile Tyr Ala Thr 520 525 530	1639
GUA GCA GGU UCU CUG UCA CUG GCA AUC AUG AUG GCU GGG AUC UCU UUC Val Ala Gly Ser Leu Ser Leu Ala Ile Met Met Ala Gly Ile Ser Phe 535 540 545	1687
UGG AUG UGC UCC AAC GGG UCU CUG CAG UGC AGG AUC UGC AUA Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile Cys Ile 550 555 560	1729
UGAUUUUAAG UCAUUUUUAU AUUAAAACA CCCUUGUUUC UACU	1773

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Asp 1 5 10 15
Lys Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Thr Val Asp 20 25 30
Thr Asn Leu Glu Arg Asn Val Thr Val Thr His Ala Lys Asp Ile Leu 35 40 45
Glu Lys Thr His Asn Gly Lys Leu Cys Lys Leu Asn Gly Ile Pro Pro 50 55 60
Leu Glu Leu Gly Asp Cys Ser Ile Ala Gly Trp Leu Leu Gly Asn Pro 65 70 75 80
Glu Cys Asp Arg Leu Leu Ser Val Pro Glu Trp Ser Tyr Ile Met Glu 85 90 95
Lys Glu Asn Pro Arg Asn Gly Leu Cys Tyr Pro Gly Asn Phe Asn Asp 100 105 110

Tyr Glu Glu Leu Lys His Leu Leu Ser Ser Val Lys His Phe Glu Lys
115 120 125

Val Lys Ile Leu Pro Lys Asp Arg Trp Ala Gln His Thr Thr Thr Gly
130 135 140

Gly Ser Gln Ala Cys Ala Val Ser Gly Asn Pro Ser Phe Phe Arg Asn
145 150 155 160

Met Val Trp Leu Thr Glu Glu Gly Ser Asn Tyr Pro Val Ala Lys Gly
165 170 175

Ser Tyr Asn Asn Thr Ser Gly Glu Gln Met Leu Ile Ile Trp Gly Val
180 185 190

His His Pro Ile Asp Glu Thr Glu Gln Arg Thr Leu Tyr Gln Asn Val
195 200 205

Gly Thr Tyr Val Ser Val Gly Thr Ser Thr Leu Asn Lys Arg Ser Thr
210 215 220

Pro Glu Ile Ala Lys Arg Pro Lys Val Asn Gly Leu Gly Ser Arg Met
225 230 235 240

Glu Phe Ser Trp Thr Leu Leu Asp Met Trp Asp Thr Ile Asn Phe Glu
245 250 255

Ser Thr Gly Asn Leu Ile Ala Pro Glu Tyr Gly Phe Lys Ile Ser Lys
260 265 270

Arg Gly Ser Ser Gly Ile Met Lys Thr Glu Gly Thr Leu Glu Asn Cys
275 280 285

Glu Thr Lys Cys Gln Thr Pro Leu Gly Ala Ile Asn Thr Thr Leu Pro
290 295 300

Phe His Asn Val His Pro Leu Thr Ile Gly Glu Cys Pro Lys Tyr Val
305 310 315 320

Lys Ser Glu Lys Leu Val Leu Ala Thr Gly Leu Arg Asn Val Pro Gln
325 330 335

Ile Glu Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly
340 345 350

Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His Ser Asn
355 360 365

Asp Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala
370 375 380

Phe Asp Gly Ile Thr Asn Lys Val Asn Ser Val Ile Glu Lys Ile Asn
385 390 395 400

Thr Gln Phe Glu Ala Val Gly Lys Glu Phe Ser Asn Leu Glu Arg Arg

405

410

415

Leu Glu Asn Leu Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp
420 425 430

Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu
435 440 445

Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr Asp Lys Val Arg Met
450 455 460

Gln Leu Arg Asp Asn Val Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe
465 470 475 480

Tyr His Lys Cys Asp Asp Glu Cys Met Asn Ser Val Lys Asn Gly Thr
485 490 495

Tyr Asp Tyr Pro Lys Tyr Glu Glu Ser Lys Leu Asn Arg Asn Glu
500 505 510

Ile Lys Gly Val Lys Leu Ser Ser Met Gly Val Cys Arg Ile Leu Ala
515 520 525

Ile Tyr Ala Thr Val Ala Gly Ser Leu Ser Leu Ala Ile Met Met Ala
530 535 540

Gly Ile Ser Phe Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile
545 550 555 560

Cys Ile

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

(B) CLONE: NA

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(394, "c")

(D) OTHER INFORMATION: /product= "Neuraminidase"
/gene= "NA"
/note= "u in ca "master" strain; c in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(604, "a")

(D) OTHER INFORMATION: /product= "Neuraminidase"
/gene= "NA"
/note= "u in ca "master" strain; a in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 20..1426

(D) OTHER INFORMATION: /product= "neuraminidase"
/gene= "NA"
/note= "neuraminidase protein"
/citation= ([1])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) Influenza Virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:37: FROM 1 TO 1467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AGCAAAAGCA GGAGUGAAA AUG AAU CCA AAU CAA AAG ACA AUA ACA AUU GGC Met Asn Pro Asn Gln Lys Thr Ile Thr Ile Gly 1 5 10	52
UCU GUC UCU CUC ACC AUC GCA ACA GUA UGC UUC CUC AUG CAG AUU GCC Ser Val Ser Leu Thr Ile Ala Thr Val Cys Phe Leu Met Gln Ile Ala 15 20 25	100
AUC CUG GCA ACU ACU GUG ACA UUG CAC CUU AAG CAA CAU GAG UGC GAC Ile Leu Ala Thr Thr Val Thr Leu His Leu Lys Gln His Glu Cys Asp 30 35 40	148
UCC CCC GCG AGC AAC CAA GUA AUG CCA UGU GAA CCA AUA AUA AUA GAA Ser Pro Ala Ser Asn Gln Val Met Pro Cys Glu Pro Ile Ile Ile Glu 45 50 55	196
AGG AAC AUA ACA GAG AUA GUG UAU UUG AAU AAC ACC ACC AUA GAG AAA Arg Asn Ile Thr Glu Ile Val Tyr Leu Asn Asn Thr Thr Ile Glu Lys 60 65 70 75	244
GAG AUU UGC CCC GAA GUA GUG GGA UAC AGA AAU UGG UCA AAG CCG CAA Glu Ile Cys Pro Glu Val Val Gly Tyr Arg Asn Trp Ser Lys Pro Gln 80 85 90	292
UGU CAA AUU ACA GGA UUU GCA CCU UUU UCU AAG GAC AAU UCA AUC CGG Cys Gln Ile Thr Gly Phe Ala Pro Phe Ser Lys Asp Asn Ser Ile Arg 95 100 105	340
CUU UCU GCU GGU GGG GAC AUU UGG GUG ACG AGA GAA CCU UAU GUG UCA Leu Ser Ala Gly Gly Asp Ile Trp Val Thr Arg Glu Pro Tyr Val Ser 110 115 120	388
UGC GAC CCU GGC AAG UGU UAU CAA UUU GCA CUC GGG CAG GGG ACC ACA Cys Asp Pro Gly Lys Cys Tyr Gln Phe Ala Leu Gly Gln Gly Thr Thr 125 130 135	436
CUA GAC AAC AAA CAU UCA AAU GGC ACA AUA CAU GAU AGA AUC CCU CAU Leu Asp Asn Lys His Ser Asn Gly Thr Ile His Asp Arg Ile Pro His 140 145 150 155	484
CGA ACC CUA UUA AUG AAU GAG UUG GGU GUU CCA UUU CAU UUA GGA ACC Arg Thr Leu Leu Met Asn Glu Leu Gly Val Pro Phe His Leu Gly Thr 160 165 170	532
AAA CAA GUG UGU GCA GCA UGG UCC AGC UCA AGU UGU CAC GAU GGA AAA Lys Gln Val Cys Ala Ala Trp Ser Ser Ser Cys His Asp Gly Lys 175 180 185	580

GCA UGG UUG CAU GUU UGU GUC ACA GGG GAU GAU AGA AAU GCA ACU GCU Ala Trp Leu His Val Cys Val Thr Gly Asp Asp Arg Asn Ala Thr Ala 190 195 200	628
AGC UUC AUU UAU GAC GGG AAG CUU GUG GAC AGU AUU GGU UCA UGG UCU Ser Phe Ile Tyr Asp Gly Lys Leu Val Asp Ser Ile Gly Ser Trp Ser 205 210 215	676
CAA AAU GUC CUC AGG ACC CAG GAG UCG GAA UGC GUC UGU AUC AAU GGG Gln Asn Val Leu Arg Thr Gln Glu Ser Glu Cys Val Cys Ile Asn Gly 220 225 230 235	724
ACU UGC ACA GUA GUA AUG ACU GAU GGA AGU GCA UCA GGA AGA GCU GAU Thr Cys Thr Val Val Met Thr Asp Gly Ser Ala Ser Gly Arg Ala Asp 240 245 250	772
ACU AGA AUA CUA UUC AUU AAA GAG GGG AAA AUU GUC CAU AUU GGC CCA Thr Arg Ile Leu Phe Ile Lys Glu Gly Lys Ile Val His Ile Gly Pro 255 260 265	820
UUG UCA GGA AGU GCU CAG CAU GUA GAG GAG UGU UCU UGU UAC CCU CGA Leu Ser Gly Ser Ala Gln His Val Glu Glu Cys Ser Cys Tyr Pro Arg 270 275 280	868
UAU CCU GAC GUC AGA UGU AUC UGC AGA GAC AAC UGG AAA GGC UCU AAU Tyr Pro Asp Val Arg Cys Ile Cys Arg Asp Asn Trp Lys Gly Ser Asn 285 290 295	916
AGG CCC GUU AUA GAC AUA AAU AUG GAA GAU UAU AGC AUU GAU UCC AGU Arg Pro Val Ile Asp Ile Asn Met Glu Asp Tyr Ser Ile Asp Ser Ser 300 305 310 315	964
UAU GUG UGC UCA GGG CUU GUU GGC GAC ACA CCC AGG AAC GAC GAC AGC Tyr Val Cys Ser Gly Leu Val Gly Asp Thr Pro Arg Asn Asp Asp Ser 320 325 330	1012
UCU AGC AAU AGC AAU UGC AGG GAU CCU AAC AAU GAG AGA GGG AAU CCA Ser Ser Asn Ser Asn Cys Arg Asp Pro Asn Asn Glu Arg Gly Asn Pro 335 340 345	1060
GGA GUG AAA GGC UGG GCC UUU GAC AAU GGA GAU GAU GUA UGG AUG GGA Gly Val Lys Gly Trp Ala Phe Asp Asn Gly Asp Asp Val Trp Met Gly 350 355 360	1108
AGA ACA AUC AGC AAA GAU UUA CGC UCA GGU UAU GAA ACU UUC AAA GUC Arg Thr Ile Ser Lys Asp Leu Arg Ser Gly Tyr Glu Thr Phe Lys Val 365 370 375	1156
AUU GGU GGU UGG UCC ACA CCU AAU UCC AAA UCG CAG GUC AAU AGA CAG Ile Gly Gly Trp Ser Thr Pro Asn Ser Lys Ser Gln Val Asn Arg Gln 380 385 390 395	1204
GUC AUA GUU GAC AAC AAU AAU UGG UCU GGU UAC UCU GGU AAU UUC UCU Val Ile Val Asp Asn Asn Asn Trp Ser Gly Tyr Ser Gly Ile Phe Ser 400 405 410	1252

GUU GAG GGC AAA AGC UGC AUC AAU AGG UGC UUU UAU GUG GAG UUG AUA
Val Glu Gly Lys Ser Cys Ile Asn Arg Cys Phe Tyr Val Glu Leu Ile
415 420 425

AGG GGA AGG CCA CAG GAG ACU AGA GUA UGG UGG ACC UCA AAC AGU AUU
Arg Gly Arg Pro Gln Glu Thr Arg Val Trp Trp Thr Ser Asn Ser Ile
430 435 440

GUU GUA UUU UGU GGC ACU UCA GGU ACU UAU GGA ACA GGC UCA UGG CCU
Val Val Phe Cys Gly Thr Ser Gly Thr Tyr Gly Thr Gly Ser Trp Pro
445 450 455

GAU GGG GCG AAC AUC AAU UUC AUG CCU AUA UAACGUUUCG CAAUUUUAGA
Asp Gly Ala Asn Ile Asn Phe Met Pro Ile
460 465

AAAAAACUCC UUGUUUCUAC U

1300
1348
1396
1446
1467

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Asn Pro Asn Gln Lys Thr Ile Thr Ile Gly Ser Val Ser Leu Thr
1 5 10 15

Ile Ala Thr Val Cys Phe Leu Met Gln Ile Ala Ile Leu Ala Thr Thr
20 25 30

Val Thr Leu His Leu Lys Gln His Glu Cys Asp Ser Pro Ala Ser Asn
35 40 45

Gln Val Met Pro Cys Glu Pro Ile Ile Glu Arg Asn Ile Thr Glu
50 55 60

Ile Val Tyr Leu Asn Asn Thr Thr Ile Glu Lys Glu Ile Cys Pro Glu
65 70 75 80

Val Val Gly Tyr Arg Asn Trp Ser Lys Pro Gln Cys Gln Ile Thr Gly
85 90 95

Phe Ala Pro Phe Ser Lys Asp Asn Ser Ile Arg Leu Ser Ala Gly Gly

100

105

110

Asp Ile Trp Val Thr Arg Glu Pro Tyr Val Ser Cys Asp Pro Gly Lys
115 120 125

Cys Tyr Gln Phe Ala Leu Gly Gln Gly Thr Thr Leu Asp Asn Lys His
130 135 140

Ser Asn Gly Thr Ile His Asp Arg Ile Pro His Arg Thr Leu Leu Met
145 150 155 160

Asn Glu Leu Gly Val Pro Phe His Leu Gly Thr Lys Gln Val Cys Ala
165 170 175

Ala Trp Ser Ser Ser Cys His Asp Gly Lys Ala Trp Leu His Val
180 185 190

Cys Val Thr Gly Asp Asp Arg Asn Ala Thr Ala Ser Phe Ile Tyr Asp
195 200 205

Gly Lys Leu Val Asp Ser Ile Gly Ser Trp Ser Gln Asn Val Leu Arg
210 215 220

Thr Gln Glu Ser Glu Cys Val Cys Ile Asn Gly Thr Cys Thr Val Val
225 230 235 240

Met Thr Asp Gly Ser Ala Ser Gly Arg Ala Asp Thr Arg Ile Leu Phe
245 250 255

Ile Lys Glu Gly Lys Ile Val His Ile Gly Pro Leu Ser Gly Ser Ala
260 265 270

Gln His Val Glu Glu Cys Ser Cys Tyr Pro Arg Tyr Pro Asp Val Arg
275 280 285

Cys Ile Cys Arg Asp Asn Trp Lys Gly Ser Asn Arg Pro Val Ile Asp
290 295 300

Ile Asn Met Glu Asp Tyr Ser Ile Asp Ser Ser Tyr Val Cys Ser Gly
305 310 315 320

Leu Val Gly Asp Thr Pro Arg Asn Asp Asp Ser Ser Ser Asn Ser Asn
325 330 335

Cys Arg Asp Pro Asn Asn Glu Arg Gly Asn Pro Gly Val Lys Gly Trp
340 345 350

Ala Phe Asp Asn Gly Asp Asp Val Trp Met Gly Arg Thr Ile Ser Lys
355 360 365

Asp Leu Arg Ser Gly Tyr Glu Thr Phe Lys Val Ile Gly Gly Trp Ser
370 375 380

Thr Pro Asn Ser Lys Ser Gln Val Asn Arg Gln Val Ile Val Asp Asn
385 390 395 400

Asn Asn Trp Ser Gly Tyr Ser Gly Ile Phe Ser Val Glu Gly Lys Ser
405 410 415

Cys Ile Asn Arg Cys Phe Tyr Val Glu Leu Ile Arg Gly Arg Pro Gln
420 425 430

Glu Thr Arg Val Trp Trp Thr Ser Asn Ser Ile Val Val Phe Cys Gly
435 440 445

Thr Ser Gly Thr Tyr Gly Thr Gly Ser Trp Pro Asp Gly Ala Asn Ile
450 455 460

Asn Phe Met Pro Ile
465

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: NP

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(113, "a")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain; a in wt2(3); c in 1988 reported wild type E28-32 strain (manuscript) but a in 1988 reported wild type E28-32 strain

/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(146, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(627, "c")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain and in wt2(3); a in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(909, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in wt2(3); c in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1550, "a")
- (D) OTHER INFORMATION: /note= "a in ca "master" strain and in wt2(3); deletion in 1988 reported wild type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 46..1539

(D) OTHER INFORMATION: /product= "Nucleoprotein"
/gene= "NP"
/note= "nucleoprotein"
/citation= ([1][2])

a)\n(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R W

(B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:39: FROM 1 TO 1566

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza vaccine strain, A/Ann Arbor/6/60 (H2N2)

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:39: FROM 1 TO 1566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGCAAAAGCA GGGUAGAUAA UCACUCACUG AGUGACAUCA AAAUC AUG GCG UCC
Met Ala Ser

CAA GGC ACC AAA CGG UCU UAU GAA CAG AUG GAA ACU GAU GGG GAA CGC Gln Gly Thr Lys Arg Ser Tyr Glu Gln Met Glu Thr Asp Gly Glu Arg 5 10 15	102
CAG AAU GCA AAU GAA AUC AGA GCA UCC GUC GGG AAG AUG AUU GGU GGA Gln Asn Ala Asn Glu Ile Arg Ala Ser Val Gly Lys Met Ile Gly Gly 20 25 30 35	150
AUU GGA CGA UUC UAC AUC CAA AUG UGC ACC GAA CUU AAA CUC AGU GAU Ile Gly Arg Phe Tyr Ile Gln Met Cys Thr Glu Leu Lys Leu Ser Asp 40 45 50	198
UAU GAG GGG CGG CUG AUC CAG AAC AGC UUA ACA AUA GAG AGA AUG GUG Tyr Glu Gly Arg Leu Ile Gln Asn Ser Leu Thr Ile Glu Arg Met Val 55 60 65	246
CUC UCU GCU UUU GAC GAG AGG AGG AAU AAA UAU CUG GAA GAA CAU CCC Leu Ser Ala Phe Asp Glu Arg Arg Asn Lys Tyr Leu Glu Glu His Pro 70 75 80	294
AGC GCG GGG AAG GAU CCU AAG AAA ACU GGA GGA CCC AUA UAC AAG AGA Ser Ala Gly Lys Asp Pro Lys Lys Thr Gly Pro Ile Tyr Lys Arg 85 90 95	342
GUA GAU GGA AAG UGG AUG AGG GAA CUC GUC CUU UAU GAC AAA GAA GAA Val Asp Gly Lys Trp Met Arg Glu Leu Val Leu Tyr Asp Lys Glu Glu 100 105 110 115	390
AUA AGG CGA AUC UGG CGC CAA GCU AAU AAU GGU GAU GAU GCA ACA GCU Ile Arg Arg Ile Trp Arg Gln Ala Asn Asn Gly Asp Asp Ala Thr Ala 120 125 130	438
GGU CUG ACU CAC AUG AUG AUC UGG CAU UCC AAU UUG AAU GAU ACA ACA Gly Leu Thr His Met Met Ile Trp His Ser Asn Leu Asn Asp Thr Thr 135 140 145	486
UAC CAG AGG ACA AGA GCU CUU GUU CGC ACC GGA AUG GAU CCC AGG AUG Tyr Gln Arg Thr Arg Ala Leu Val Arg Thr Gly Met Asp Pro Arg Met 150 155 160	534
UGC UCU UUG AUG CAG GGU UCG ACU CUC CCU AGG AGG UCU GGA GCC GCA Cys Ser Leu Met Gln Gly Ser Thr Leu Pro Arg Arg Ser Gly Ala Ala 165 170 175	582
GGC GCU GCA GUC AAA GGA GUU GGG ACA AUG GUG AUG GAG UUG AUC AGG Gly Ala Ala Val Lys Gly Val Gly Thr Met Val Met Glu Leu Ile Arg 180 185 190 195	630
AUG AUC AAA CGU GGG AUC AAU GAU CGG AAC UUC UGG AGA GGU GAG AAU Met Ile Lys Arg Gly Ile Asn Asp Arg Asn Phe Trp Arg Gly Glu Asn 200 205 210	678
GGG CGG AAA ACA AGG AAU GCU UAU GAG AGA AUG UGC AAC AUU CUC AAA Gly Arg Lys Thr Arg Asn Ala Tyr Glu Arg Met Cys Asn Ile Leu Lys 215 220 225	726

GGA AAA UUU CAA ACA GCU GCA CAA AGA GCA AUG AUG GAU CAA GUG AGA Gly Lys Phe Gln Thr Ala Ala Gln Arg Ala Met Met Asp Gln Val Arg 230 235 240	774
GAA AGC CGG AAC CCA GGA AAU GCU GAG AUC GAA GAU CUC AUC UUU CUG Glu Ser Arg Asn Pro Gly Asn Ala Glu Ile Glu Asp Leu Ile Phe Leu 245 250 255	822
GCA CGG UCU GCA CUC AUA UUG AGA GGG UCA GUU GCU CAC AAA UCU UGU Ala Arg Ser Ala Leu Ile Leu Arg Gly Ser Val Ala His Lys Ser Cys 260 265 270 275	870
CUG CCU GCC UGU GUG UAU GGA CCU GCC GUA GCC AGU GGG UAC GAC UUC Leu Pro Ala Cys Val Tyr Gly Pro Ala Val Ala Ser Gly Tyr Asp Phe 280 285 290	918
GAA AAA GAG GGA UAC UCU UUA GUA GGG AUA GAC CCA UUC AAA CUG CUU Glu Lys Glu Gly Tyr Ser Leu Val Gly Ile Asp Pro Phe Lys Leu Leu 295 300 305	966
CAA AAC AGC CAA GUA UAC AGC CUA AUC AGA CCG AAU GAG AAU CCA GCA Gln Asn Ser Gln Val Tyr Ser Leu Ile Arg Pro Asn Glu Asn Pro Ala 310 315 320	1014
CAC AAG AGU CAG CUG GUG UGG AUG GCA UGC AAU UCU GCU GCA UUU GAA His Lys Ser Gln Leu Val Trp Met Ala Cys Asn Ser Ala Ala Phe Glu 325 330 335	1062
GAU CUA AGA GUA UCA AGC UUC AUC AGA GGG ACC AAA GUA AUC CCA AGG Asp Leu Arg Val Ser Ser Phe Ile Arg Gly Thr Lys Val Ile Pro Arg 340 345 350 355	1110
GGG AAA CUU UCC ACU AGA GGA GUA CAA AUU GCU UCA AAU GAA AAC AUG Gly Lys Leu Ser Thr Arg Gly Val Gln Ile Ala Ser Asn Glu Asn Met 360 365 370	1158
GAU ACU AUG GGA UCA AGU ACU CUU GAA CUG AGA AGC AGG UAC UGG GCC Asp Thr Met Gly Ser Ser Thr Leu Glu Leu Arg Ser Arg Tyr Trp Ala 375 380 385	1206
AUA AGG ACC AGA AGU GGA GGA AAC ACU AAU CAA CAG AGG GCC UCU GCA Ile Arg Thr Arg Ser Gly Gly Asn Thr Asn Gln Gln Arg Ala Ser Ala 390 395 400	1254
GGU CAA AUC AGU GUA CAA CCU ACG UUU UCU GUG CAA AGA AAC CUC CCA Gly Gln Ile Ser Val Gln Pro Thr Phe Ser Val Gln Arg Asn Leu Pro 405 410 415	1302
UUU GAC AAA CCA ACC AUC AUG GCA GCA UUC ACU GGG AAU GCA GAG GGA Phe Asp Lys Pro Thr Ile Met Ala Ala Phe Thr Gly Asn Ala Glu Gly 420 425 430 435	1350
AGA ACA UCA GAC AUG AGG GCA GAA AUC AUA AGG AUG AUG GAA GGU GCA Arg Thr Ser Asp Met Arg Ala Glu Ile Ile Arg Met Met Glu Gly Ala 440 445 450	1398

AAA CCA GAA GAA GUG UCC UUC CAG GGG CGG GGA GUC UUC GAG CUC UCG Lys Pro Glu Glu Val Ser Phe Gln Gly Arg Gly Val Phe Glu Leu Ser 455 460 465	1446
GAC GAA AAG GCA ACG AAC CCG AUC GUG CCC UCU UUU GAC AUG AGU AAU Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp Met Ser Asn 470 475 480	1494
GAA GGA UCU UAU UUC UUC GGA GAC AAU GCA GAG GAG UAC GAC AAU Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr Asp Asn 485 490 495	1539
UAAGGAAAAA AUACCCUUGU UUCUACU	1566

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Ala Ser Gln Gly Thr Lys Arg Ser Tyr Glu Gln Met Glu Thr Asp 1 5 10 15
Gly Glu Arg Gln Asn Ala Asn Glu Ile Arg Ala Ser Val Gly Lys Met 20 25 30
Ile Gly Gly Ile Gly Arg Phe Tyr Ile Gln Met Cys Thr Glu Leu Lys 35 40 45
Leu Ser Asp Tyr Glu Gly Arg Leu Ile Gln Asn Ser Leu Thr Ile Glu 50 55 60
Arg Met Val Leu Ser Ala Phe Asp Glu Arg Arg Asn Lys Tyr Leu Glu 65 70 75 80
Glu His Pro Ser Ala Gly Lys Asp Pro Lys Lys Thr Gly Gly Pro Ile 85 90 95
Tyr Lys Arg Val Asp Gly Lys Trp Met Arg Glu Leu Val Leu Tyr Asp 100 105 110
Lys Glu Glu Ile Arg Arg Ile Trp Arg Gln Ala Asn Asn Gly Asp Asp 115 120 125

Ala Thr Ala Gly Leu Thr His Met Met Ile Trp His Ser Asn Leu Asn
130 135 140

Asp Thr Thr Tyr Gln Arg Thr Arg Ala Leu Val Arg Thr Gly Met Asp
145 150 155 160

Pro Arg Met Cys Ser Leu Met Gln Gly Ser Thr Leu Pro Arg Arg Ser
165 170 175

Gly Ala Ala Gly Ala Ala Val Lys Gly Val Gly Thr Met Val Met Glu
180 185 190

Leu Ile Arg Met Ile Lys Arg Gly Ile Asn Asp Arg Asn Phe Trp Arg
195 200 205

Gly Glu Asn Gly Arg Lys Thr Arg Asn Ala Tyr Glu Arg Met Cys Asn
210 215 220

Ile Leu Lys Gly Lys Phe Gln Thr Ala Ala Gln Arg Ala Met Met Asp
225 230 235 240

Gln Val Arg Glu Ser Arg Asn Pro Gly Asn Ala Glu Ile Glu Asp Leu
245 250 255

Ile Phe Leu Ala Arg Ser Ala Leu Ile Leu Arg Gly Ser Val Ala His
260 265 270

Lys Ser Cys Leu Pro Ala Cys Val Tyr Gly Pro Ala Val Ala Ser Gly
275 280 285

Tyr Asp Phe Glu Lys Glu Gly Tyr Ser Leu Val Gly Ile Asp Pro Phe
290 295 300

Lys Leu Leu Gln Asn Ser Gln Val Tyr Ser Leu Ile Arg Pro Asn Glu
305 310 315 320

Asn Pro Ala His Lys Ser Gln Leu Val Trp Met Ala Cys Asn Ser Ala
325 330 335

Ala Phe Glu Asp Leu Arg Val Ser Ser Phe Ile Arg Gly Thr Lys Val
340 345 350

Ile Pro Arg Gly Lys Leu Ser Thr Arg Gly Val Gln Ile Ala Ser Asn
355 360 365

Glu Asn Met Asp Thr Met Gly Ser Ser Thr Leu Glu Leu Arg Ser Arg
370 375 380

Tyr Trp Ala Ile Arg Thr Arg Ser Gly Gly Asn Thr Asn Gln Gln Arg
385 390 395 400

Ala Ser Ala Gly Gln Ile Ser Val Gln Pro Thr Phe Ser Val Gln Arg
405 410 415

Asn Leu Pro Phe Asp Lys Pro Thr Ile Met Ala Ala Phe Thr Gly Asn

420

425

430

Ala Glu Gly Arg Thr Ser Asp Met Arg Ala Glu Ile Ile Arg Met Met
435 440 445

Glu Gly Ala Lys Pro Glu Glu Val Ser Phe Gln Gly Arg Gly Val Phe
450 455 460

Glu Leu Ser Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp
465 470 475 480

Met Ser Asn Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr
485 490 495

Asp Asn